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<110> Genentech, Inc.
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 Eaton, Dan L.
 Ferrara, Napoleone
 Filvaroff, Ellen
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 Gao, Wei-Qiang
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 Goddard, A.
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 Pan, James
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Stewart, Timothy A.
 Tumas, Daniel
 Williams, P. Mickey
 Wood, William, I.

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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
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Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
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Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
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Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
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Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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| Ala | Glu | Tyr | Phe | Tyr | Glu | Phe | Leu | Ser | Leu | Arg | Ser | Leu | Asp | Lys | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
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|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Glu | Arg | Arg | Ile | Cys | Glu | Cys | Pro | Asp | Gly | Phe | His | Gly | Pro | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
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|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Thr | Pro | Gly | Phe | Cys | Ile | Cys | Pro | Pro | Gly | Phe | Tyr | Gly | Val | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Asp | Lys | Ala | Asn | Cys | Ser | Thr | Thr | Cys | Phe | Asn | Gly | Gly | Thr | Cys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Tyr | Pro | Gly | Lys | Cys | Ile | Cys | Pro | Pro | Gly | Leu | Glu | Gly | Glu | Gln |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
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| Ile | Gly | Lys | Ser | Lys | Cys | Lys | Cys | Ser | Lys | Gly | Tyr | Gln | Gly | Asp | Leu |
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 35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
 50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
 65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
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Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
 100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
 115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
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Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
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09905348-071204

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TOCT-20-34E0660

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Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
 180 185

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctcctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA

0905348-071304  
 TOTAL 20-24506650



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

TOCT20-2450660

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 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
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&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
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<210> 27  
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 <212> DNA  
 <213> Homo sapiens

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 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys  
20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125

09905348.0.1301

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
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 275 280 285  
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 325 330 335  
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 340 345 350  
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 355 360 365  
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 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
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0905348-071301

405 410 415  
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 Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly  
 450 455 460  
 Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu  
 465 470 475 480  
 Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu  
 485 490 495  
 Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala  
 500 505 510  
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 515 520 525  
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 Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser  
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 Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys  
 565 570 575  
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 595 600 605  
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 610 615 620  
 Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His  
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<210> 29  
 <211> 21  
 <212> DNA

TEETQ"84E50660

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggctctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Lys | Met | Leu | Ala | Gly | Cys | Phe | Leu | Leu | Ile | Leu | Gly | Gln | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Leu | Leu | Pro | Ala | Glu | Ala | Arg | Glu | Arg | Ser | Arg | Gly | Arg | Ser | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Arg | Gly | Arg | His | Ala | Arg | Thr | His | Pro | Gln | Thr | Ala | Leu | Leu | Glu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Ser | Cys | Glu | Asn | Lys | Arg | Ala | Asp | Leu | Val | Phe | Ile | Ile | Asp | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Arg | Ser | Val | Asn | Thr | His | Asp | Tyr | Ala | Lys | Val | Lys | Glu | Phe | Ile |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Val | Asp | Ile | Leu | Gln | Phe | Leu | Asp | Ile | Gly | Pro | Asp | Val | Thr | Arg | Val |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Gly | Leu | Leu | Gln | Tyr | Gly | Ser | Thr | Val | Lys | Asn | Glu | Phe | Ser | Leu | Lys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Thr | Phe | Lys | Arg | Lys | Ser | Glu | Val | Glu | Arg | Ala | Val | Lys | Arg | Met | Arg |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| His | Leu | Ser | Thr | Gly | Thr | Met | Thr | Gly | Leu | Ala | Ile | Gln | Tyr | Ala | Leu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asn | Ile | Ala | Phe | Ser | Glu | Ala | Glu | Gly | Ala | Arg | Pro | Leu | Arg | Glu | Asn |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Val | Pro | Arg | Val | Ile | Met | Ile | Val | Thr | Asp | Gly | Arg | Pro | Gln | Asp | Ser |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Val | Ala | Glu | Val | Ala | Ala | Lys | Ala | Arg | Asp | Thr | Gly | Ile | Leu | Ile | Phe |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ala | Ile | Gly | Val | Gly | Gln | Val | Asp | Phe | Asn | Thr | Leu | Lys | Ser | Ile | Gly |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Ser | Glu | Pro | His | Glu | Asp | His | Val | Phe | Leu | Val | Ala | Asn | Phe | Ser | Gln |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ile | Glu | Thr | Leu | Thr | Ser | Val | Phe | Gln | Lys | Lys | Leu | Cys | Thr | Ala | His |  |

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|                 |                     |                 |                 |     |  |     |
|-----------------|---------------------|-----------------|-----------------|-----|--|-----|
| 225             |                     | 230             |                 | 235 |  | 240 |
| Met Cys Ser Thr | Leu Glu His Asn Cys | Ala His Phe Cys | Ile Asn Ile     |     |  |     |
|                 | 245                 | 250             | 255             |     |  |     |
| Pro Gly Ser Tyr | Val Cys Arg Cys     | Lys Gln Gly Tyr | Ile Leu Asn Ser |     |  |     |
|                 | 260                 | 265             | 270             |     |  |     |
| Asp Gln Thr Thr | Cys Arg Ile Gln Asp | Leu Cys Ala Met | Glu Asp His     |     |  |     |
|                 | 275                 | 280             | 285             |     |  |     |
| Asn Cys Glu Gln | Leu Cys Val Asn Val | Pro Gly Ser Phe | Val Cys Gln     |     |  |     |
|                 | 290                 | 295             | 300             |     |  |     |
| Cys Tyr Ser Gly | Tyr Ala Leu Ala     | Glu Asp Gly Lys | Arg Cys Val Ala |     |  |     |
| 305             | 310                 | 315             | 320             |     |  |     |
| Val Asp Tyr Cys | Ala Ser Glu Asn His | Gly Cys Glu His | Glu Cys Val     |     |  |     |
|                 | 325                 | 330             | 335             |     |  |     |
| Asn Ala Asp Gly | Ser Tyr Leu Cys     | Gln Cys His Glu | Gly Phe Ala Leu |     |  |     |
|                 | 340                 | 345             | 350             |     |  |     |
| Asn Pro Asp Glu | Lys Thr Cys Thr     | Arg Ile Asn Tyr | Cys Ala Leu Asn |     |  |     |
|                 | 355                 | 360             | 365             |     |  |     |
| Lys Pro Gly Cys | Glu His Glu Cys     | Val Asn Met Glu | Glu Ser Tyr Tyr |     |  |     |
|                 | 370                 | 375             | 380             |     |  |     |
| Cys Arg Cys His | Arg Gly Tyr Thr     | Leu Asp Pro Asn | Gly Lys Thr Cys |     |  |     |
| 385             | 390                 | 395             | 400             |     |  |     |
| Ser Arg Val Asp | His Cys Ala Gln     | Gln Asp His Gly | Cys Glu Gln Leu |     |  |     |
|                 | 405                 | 410             | 415             |     |  |     |
| Cys Leu Asn Thr | Glu Asp Ser Phe     | Val Cys Gln Cys | Ser Glu Gly Phe |     |  |     |
|                 | 420                 | 425             | 430             |     |  |     |
| Leu Ile Asn Glu | Asp Leu Lys Thr     | Cys Ser Arg Val | Asp Tyr Cys Leu |     |  |     |
|                 | 435                 | 440             | 445             |     |  |     |
| Leu Ser Asp His | Gly Cys Glu Tyr     | Ser Cys Val Asn | Met Asp Arg Ser |     |  |     |
|                 | 450                 | 455             | 460             |     |  |     |
| Phe Ala Cys Gln | Cys Pro Glu Gly     | His Val Leu Arg | Ser Asp Gly Lys |     |  |     |
| 465             | 470                 | 475             | 480             |     |  |     |
| Thr Cys Ala Lys | Leu Asp Ser Cys     | Ala Leu Gly Asp | His Gly Cys Glu |     |  |     |
|                 | 485                 | 490             | 495             |     |  |     |
| His Ser Cys Val | Ser Ser Glu Asp     | Ser Phe Val Cys | Gln Cys Phe Glu |     |  |     |
|                 | 500                 | 505             | 510             |     |  |     |

0590548 "0101" 04E50660

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Tyr | Ile | Leu | Arg | Glu | Asp | Gly | Lys | Thr | Cys | Arg | Arg | Lys | Asp | Val |
|     |     | 515 |     |     |     | 520 |     |     |     | 525 |     |     |     |     |     |
| Cys | Gln | Ala | Ile | Asp | His | Gly | Cys | Glu | His | Ile | Cys | Val | Asn | Ser | Asp |
|     |     | 530 |     |     |     | 535 |     |     |     | 540 |     |     |     |     |     |
| Asp | Ser | Tyr | Thr | Cys | Glu | Cys | Leu | Glu | Gly | Phe | Arg | Leu | Ala | Glu | Asp |
|     |     |     |     | 550 |     |     |     |     |     | 555 |     |     |     | 560 |     |
| Gly | Lys | Arg | Cys | Arg | Arg | Lys | Asp | Val | Cys | Lys | Ser | Thr | His | His | Gly |
|     |     |     |     | 565 |     |     |     |     |     | 570 |     |     |     | 575 |     |
| Cys | Glu | His | Ile | Cys | Val | Asn | Asn | Gly | Asn | Ser | Tyr | Ile | Cys | Lys | Cys |
|     |     | 580 |     |     |     |     |     | 585 |     |     |     | 590 |     |     |     |
| Ser | Glu | Gly | Phe | Val | Leu | Ala | Glu | Asp | Gly | Arg | Arg | Cys | Lys | Lys | Cys |
|     |     | 595 |     |     |     | 600 |     |     |     |     |     | 605 |     |     |     |
| Thr | Glu | Gly | Pro | Ile | Asp | Leu | Val | Phe | Val | Ile | Asp | Gly | Ser | Lys | Ser |
|     |     | 610 |     |     |     | 615 |     |     |     | 620 |     |     |     |     |     |
| Leu | Gly | Glu | Glu | Asn | Phe | Glu | Val | Val | Lys | Gln | Phe | Val | Thr | Gly | Ile |
|     |     | 625 |     | 630 |     |     |     |     |     | 635 |     |     |     | 640 |     |
| Ile | Asp | Ser | Leu | Thr | Ile | Ser | Pro | Lys | Ala | Ala | Arg | Val | Gly | Leu | Leu |
|     |     |     |     | 645 |     |     |     | 650 |     |     |     |     |     | 655 |     |
| Gln | Tyr | Ser | Thr | Gln | Val | His | Thr | Glu | Phe | Thr | Leu | Arg | Asn | Phe | Asn |
|     |     | 660 |     |     |     |     |     | 665 |     |     |     | 670 |     |     |     |
| Ser | Ala | Lys | Asp | Met | Lys | Lys | Ala | Val | Ala | His | Met | Lys | Tyr | Met | Gly |
|     |     | 675 |     |     |     | 680 |     |     |     |     |     | 685 |     |     |     |
| Lys | Gly | Ser | Met | Thr | Gly | Leu | Ala | Leu | Lys | His | Met | Phe | Glu | Arg | Ser |
|     |     | 690 |     |     |     | 695 |     |     |     | 700 |     |     |     |     |     |
| Phe | Thr | Gln | Gly | Glu | Gly | Ala | Arg | Pro | Leu | Ser | Thr | Arg | Val | Pro | Arg |
|     |     | 705 |     | 710 |     |     |     |     |     | 715 |     |     |     | 720 |     |
| Ala | Ala | Ile | Val | Phe | Thr | Asp | Gly | Arg | Ala | Gln | Asp | Asp | Val | Ser | Glu |
|     |     |     |     | 725 |     |     |     | 730 |     |     |     |     |     | 735 |     |
| Trp | Ala | Ser | Lys | Ala | Lys | Ala | Asn | Gly | Ile | Thr | Met | Tyr | Ala | Val | Gly |
|     |     | 740 |     |     |     |     |     | 745 |     |     |     | 750 |     |     |     |
| Val | Gly | Lys | Ala | Ile | Glu | Glu | Glu | Leu | Gln | Glu | Ile | Ala | Ser | Glu | Pro |
|     |     | 755 |     |     |     | 760 |     |     |     |     |     | 765 |     |     |     |
| Thr | Asn | Lys | His | Leu | Phe | Tyr | Ala | Glu | Asp | Phe | Ser | Thr | Met | Asp | Glu |
|     |     | 770 |     |     |     | 775 |     |     |     | 780 |     |     |     |     |     |
| Ile | Ser | Glu | Lys | Leu | Lys | Lys | Gly | Ile | Cys | Glu | Ala | Leu | Glu | Asp | Ser |
|     |     | 785 |     | 790 |     |     |     |     |     | 795 |     |     |     | 800 |     |

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
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Arg Tyr Arg  
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<211> 23

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<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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23

<210> 36

<211> 22

<212> DNA

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

TOPFLO" SHE50660

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 37

gcctgtcagt gtccctgaggg acacgtgctc cgcagc gatg ggaag

45

&lt;210&gt; 38

&lt;211&gt; 1813

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

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tttgtatgaa aaa
1813

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&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

F005348.0 3450550

| 1                                                               | 5   | 10  | 15  |
|-----------------------------------------------------------------|-----|-----|-----|
| Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln | 20  | 25  | 30  |
| Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val | 35  | 40  | 45  |
| Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln | 50  | 55  | 60  |
| Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys | 65  | 70  | 75  |
| Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro | 85  | 90  | 95  |
| Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg | 100 | 105 | 110 |
| Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val | 115 | 120 | 125 |
| Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr | 130 | 135 | 140 |
| Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu | 145 | 150 | 155 |
| Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser | 165 | 170 | 175 |
| Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro | 180 | 185 | 190 |
| Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser | 195 | 200 | 205 |
| Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys | 210 | 215 | 220 |
| Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu | 225 | 230 | 235 |
| Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly | 245 | 250 | 255 |
| Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His | 260 | 265 | 270 |
| Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp | 275 | 280 | 285 |

FOET 20 " 84E50650

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
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Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

09054-0101-01

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 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
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 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
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 oligonucleotide probe  
  
 <400> 45  
 cagcagcttc agccaccagg agtgg 25  
  
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T00T20"84E50650  
 0905348-0130



<211> 45  
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<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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45

<210> 48

<211> 2822

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
 35 40 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
 50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
 65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
 85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
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Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
 115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
 130 135 140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
 145 150 155 160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
 165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

09546-071301

|                                                                 |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|
|                                                                 | 180 |     | 185 |     | 190 |
| Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val | 195 | 200 | 205 |     |     |
| Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys | 210 | 215 | 220 |     |     |
| Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe | 225 | 230 | 235 | 240 |     |
| Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys | 245 | 250 | 255 |     |     |
| Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met | 260 | 265 | 270 |     |     |
| Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala | 275 | 280 | 285 |     |     |
| Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser | 290 | 295 | 300 |     |     |
| Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln | 305 | 310 | 315 | 320 |     |
| Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile | 325 | 330 | 335 |     |     |
| Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys | 340 | 345 | 350 |     |     |
| Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser | 355 | 360 | 365 |     |     |
| Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp | 370 | 375 | 380 |     |     |
| Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser | 385 | 390 | 395 | 400 |     |
| Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly | 405 | 410 | 415 |     |     |
| Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln | 420 | 425 | 430 |     |     |
| Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr | 435 | 440 | 445 |     |     |
| Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys | 450 | 455 | 460 |     |     |

TOEFL-0-84E50660

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<210> 50
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (61)
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<223> a, t, c or g

<400> 50

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tggaacata tctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaattggca atgttgcagt tgcattttta tattataaga 120
gtattggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacgc aaaggtcaca 300
gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tggtcttcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgcctgtgt 420
aatcacctga cacattttgc aattttgatg tctctgtggtc cttccattgg tattaagat 480
tataatatcc ttacaaggat cactcaacta ggaataatta ttctactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

TOPIC: 018450660

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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cgctaagcga ggctcctcc tcccgagat ccgaacggcc tgggcgggggt caccocggct 120

TFE20"84E50650

```
<210> 59
<211> 216
<212> PRT
<213> Homo sapiens
```

```

<400> 59
Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
 1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
 50 55 60

```

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 61

gcctcccggg ctccctgagc agtgccaaac agcggcagtg ta

42

090548-0134E50660



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtcgggt gacaagccca aa

22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120  
 gctgctgctg cgctacctgg tggcgccct gggtatcat aaggcctatg gggtttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggcctatt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtggag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgcg gggaaatata gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgggaagtatt 480  
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540  
 agagctacga tgtcaagaca aagaaggga tccagctcct gaatacacat ggtttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660  
 aatgaatata aaaactggaa ctctgcaatt taatactgtt tccaaactgg aactggaga 720  
 atattcctgt gaagcccga attctgttgg atatcgagg tgcctggga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
 ttccgtttgt ggccttgggt tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900  
 ctctttccag aagagtaatt ctcatctaa agccacgaca atgagtgaat atgtgcagtg 960  
 gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020  
 gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080  
 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgaggag cggaggttgc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200  
 cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact gggtttttacc 1260  
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15  
 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
 35 40 45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
 50 55 60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
 65 70 75 80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
 85 90 95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
 100 105 110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
 115 120 125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
 130 135 140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
 145 150 155 160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
 165 170 175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
 180 185 190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
 195 200 205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
 210 215 220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
 225 230 235 240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
 245 250 255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
 260 265 270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
 275 280 285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
 290 295 300  
 Gly Gly Ser Arg Gly Gln Glu Phe

0905348-01301  
 0905348-01301

305 310

<210> 65  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 65  
 atcggtgtga agttagtgcc cc 22

<210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 66  
 acctgcgata tccaacagaa ttg 23

<210> 67  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 67  
 ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
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 agaaagaaga ggaagatggt gggcaacatt tatttaacat gctccacagc cgggacctg 120  
 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
 aaataaatga attactcaat ctctatgac catctataca tactccacct tcaaaaagta 240  
 catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300  
 ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360  
 tggcattcat catttgacaa atgcaagcat ctctcttacc aatcagctcc tattgaactt 420  
 actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480  
 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtag 540

TOEFL 2018 84250660

```

aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttggt 600
ttacacccag atccatttat atggaagcat ctacagtggg ttgtaatgat ttaggtcttt 660
taactttccc agccagattg ccagctaaca cacagattct tctcctacag actaacaata 720
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcttttctg 840
tgtacctaga ggaaaacaaa cttactgaac tgcctgaaaa atgtctgtcc gaactgagca 900
acttacaaga actctatatt aatcacaaact tgctttctac aatttcacct ggagccttta 960
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gtaagtgggt tgatgctctt ccaaacttag agattctgat gattggggaa aatccaatta 1080
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gtataaacct cacagaaata ccagataacg ccttggttgg actggaaaac ttagaaagca 1200
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atctcaaatt tttggatcta aataaaaaat ctattaatag aatacgaagg ggtgatttta 1320
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380
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atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat cctcctctga 2520
taaattctct ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580
taggtttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

```

&lt;210&gt; 69

&lt;211&gt; 708

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

```

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
 1 5 10 15

```

```

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
 20 25 30

```

```

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
 35 40 45

```

```

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
 50 55 60

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Leu | Pro | Ala | Asn | Thr | Gln | Ile | Leu | Leu | Gln | Thr | Asn | Asn |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Ala | Lys | Ile | Glu | Tyr | Ser | Thr | Asp | Phe | Pro | Val | Asn | Leu | Thr | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asp | Leu | Ser | Gln | Asn | Asn | Leu | Ser | Ser | Val | Thr | Asn | Ile | Asn | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Lys | Met | Pro | Gln | Leu | Leu | Ser | Val | Tyr | Leu | Glu | Glu | Asn | Lys | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Glu | Leu | Pro | Glu | Lys | Cys | Leu | Ser | Glu | Leu | Ser | Asn | Leu | Gln | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Tyr | Ile | Asn | His | Asn | Leu | Leu | Ser | Thr | Ile | Ser | Pro | Gly | Ala | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Gly | Leu | His | Asn | Leu | Leu | Arg | Leu | His | Leu | Asn | Ser | Asn | Arg | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Met | Ile | Asn | Ser | Lys | Trp | Phe | Asp | Ala | Leu | Pro | Asn | Leu | Glu | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Met | Ile | Gly | Glu | Asn | Pro | Ile | Ile | Arg | Ile | Lys | Asp | Met | Asn | Phe |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Lys | Pro | Leu | Ile | Asn | Leu | Arg | Ser | Leu | Val | Ile | Ala | Gly | Ile | Asn | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Glu | Ile | Pro | Asp | Asn | Ala | Leu | Val | Gly | Leu | Glu | Asn | Leu | Glu | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Ser | Phe | Tyr | Asp | Asn | Arg | Leu | Ile | Lys | Val | Pro | His | Val | Ala | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Lys | Val | Val | Asn | Leu | Lys | Phe | Leu | Asp | Leu | Asn | Lys | Asn | Pro | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Arg | Ile | Arg | Arg | Gly | Asp | Phe | Ser | Asn | Met | Leu | His | Leu | Lys | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Gly | Ile | Asn | Asn | Met | Pro | Glu | Leu | Ile | Ser | Ile | Asp | Ser | Leu | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Asp | Asn | Leu | Pro | Asp | Leu | Arg | Lys | Ile | Glu | Ala | Thr | Asn | Asn | Pro |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Leu | Ser | Tyr | Ile | His | Pro | Asn | Ala | Phe | Phe | Arg | Leu | Pro | Lys | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Ser | Leu | Met | Leu | Asn | Ser | Asn | Ala | Leu | Ser | Ala | Leu | Tyr | His | Gly |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 340 |     | 345 |     | 350 |     |     |     |     |     |     |     |     |     |     |
| Thr | Ile | Glu | Ser | Leu | Pro | Asn | Leu | Lys | Glu | Ile | Ser | Ile | His | Ser | Asn |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Pro | Ile | Arg | Cys | Asp | Cys | Val | Ile | Arg | Trp | Met | Asn | Met | Asn | Lys | Thr |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asn | Ile | Arg | Phe | Met | Glu | Pro | Asp | Ser | Leu | Phe | Cys | Val | Asp | Pro | Pro |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Glu | Phe | Gln | Gly | Gln | Asn | Val | Arg | Gln | Val | His | Phe | Arg | Asp | Met | Met |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Glu | Ile | Cys | Leu | Pro | Leu | Ile | Ala | Pro | Glu | Ser | Phe | Pro | Ser | Asn | Leu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Asn | Val | Glu | Ala | Gly | Ser | Tyr | Val | Ser | Phe | His | Cys | Arg | Ala | Thr | Ala |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Pro | Gln | Pro | Glu | Ile | Tyr | Trp | Ile | Thr | Pro | Ser | Gly | Gln | Lys | Leu |
|     | 450 |     |     |     |     | 455 |     |     |     |     |     | 460 |     |     |     |
| Leu | Pro | Asn | Thr | Leu | Thr | Asp | Lys | Phe | Tyr | Val | His | Ser | Glu | Gly | Thr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Leu | Asp | Ile | Asn | Gly | Val | Thr | Pro | Lys | Glu | Gly | Gly | Leu | Tyr | Thr | Cys |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Ile | Ala | Thr | Asn | Leu | Val | Gly | Ala | Asp | Leu | Lys | Ser | Val | Met | Ile | Lys |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Val | Asp | Gly | Ser | Phe | Pro | Gln | Asp | Asn | Asn | Gly | Ser | Leu | Asn | Ile | Lys |
|     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Ile | Arg | Asp | Ile | Gln | Ala | Asn | Ser | Val | Leu | Val | Ser | Trp | Lys | Ala | Ser |
|     | 530 |     |     |     |     | 535 |     |     |     |     |     | 540 |     |     |     |
| Ser | Lys | Ile | Leu | Lys | Ser | Ser | Val | Lys | Trp | Thr | Ala | Phe | Val | Lys | Thr |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Glu | Asn | Ser | His | Ala | Ala | Gln | Ser | Ala | Arg | Ile | Pro | Ser | Asp | Val | Lys |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Val | Tyr | Asn | Leu | Thr | His | Leu | Asn | Pro | Ser | Thr | Glu | Tyr | Lys | Ile | Cys |
|     |     | 580 |     |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Ile | Asp | Ile | Pro | Thr | Ile | Tyr | Gln | Lys | Asn | Arg | Lys | Lys | Cys | Val | Asn |
|     | 595 |     |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Val | Thr | Thr | Lys | Gly | Leu | His | Pro | Asp | Gln | Lys | Glu | Tyr | Glu | Lys | Asn |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |

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Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 70  
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ttaccacgct tggtggagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180  
gaatctggta gacctgtggt taaccctgtt cctctccatg tgtctcctcc tacaagttt 240  
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggt gtctttgttc 300  
ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360  
tcttctctct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420  
tgaaatTTTT aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480  
gtttatcgat gagcatgctt tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540  
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccaggggccag 600  
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cctgccaaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960  
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<210> 71  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 71

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 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

FOOTNOTES: 071304



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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accgagccga gcggaaccga ggcgcgcgcg agatgcaggt gagcaagagg atgctggcgg 60
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cccaggaccg cgtgtgtgtg tgcacccgca agtgetttgt ggcagtcccc gagggcatcc 240
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gcctgaagct catcccgtca ggcgtcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcggt atcctactgg actacatggt tcaggacctg tacaacctca 540
agtcactgga ggttggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcgggc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgccc tgaggtccg gcacctcaac atcaatgcca 720
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cgggcggccg ggcaggggaa ggggcctggt cgcacactgc tcaactctca gtcttccca 1980
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aaaaaaaaaa 2290

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&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

```

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
 1 5 10 15

```

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
 20 25 30  
 Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35 40 45  
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95  
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100 105 110  
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115 120 125  
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130 135 140  
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145 150 155 160  
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165 170 175  
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180 185 190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300

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Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
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 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

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 T00T20" 84E50660

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 580 |     | 585 |     | 590 |     |     |     |     |     |     |     |     |     |     |
| Ile | Glu | Ile | Glu | Tyr | Val | Pro | Arg | Lys | Ser | Asp | Ala | Gly | Ile | Ser | Ser |
|     | 595 |     |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Ala | Asp | Ala | Pro | Arg | Lys | Phe | Asn | Met | Lys | Met | Ile |     |     |     |     |
|     | 610 |     |     |     |     |     | 615 |     |     |     | 620 |     |     |     |     |

<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 74  
 tcacctggag cctttattgg cc 22

<210> 75  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 75  
 ataccagcta taaccaggct gcg 23

<210> 76  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 76  
 caacagtaag tggtttgatg ctcttcctaaa tctagagatt ctgatgattg 50  
 gg 52

<210> 77  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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24

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 acatcgtagt ccacccccctc cccatcccca gcccccgggg attcaggctc gccagcgccc 120  
 agccagggag ccggccggga agcgcgatgg gggccccagc cgctcgctc ctgctcctgc 180  
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 ccctttccgt ggcttctctg catttggggt attattatt ttgtaacaat cccaaatcaa 1620  
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 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Pro | Ala | Ala | Ser | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Phe | Ala | 1   | 5   | 10  | 15  |
| Cys | Cys | Trp | Ala | Pro | Gly | Gly | Ala | Asn | Leu | Ser | Gln | Asp | Asp | Ser | Gln | 20  | 25  | 30  |     |
| Pro | Trp | Thr | Ser | Asp | Glu | Thr | Val | Val | Ala | Gly | Gly | Thr | Val | Val | Leu | 35  | 40  | 45  |     |
| Lys | Cys | Gln | Val | Lys | Asp | His | Glu | Asp | Ser | Ser | Leu | Gln | Trp | Ser | Asn | 50  | 55  | 60  |     |
| Pro | Ala | Gln | Gln | Thr | Leu | Tyr | Phe | Gly | Glu | Lys | Arg | Ala | Leu | Arg | Asp | 65  | 70  | 75  | 80  |
| Asn | Arg | Ile | Gln | Leu | Val | Thr | Ser | Thr | Pro | His | Glu | Leu | Ser | Ile | Ser | 85  | 90  | 95  |     |
| Ile | Ser | Asn | Val | Ala | Leu | Ala | Asp | Glu | Gly | Glu | Tyr | Thr | Cys | Ser | Ile | 100 | 105 | 110 |     |
| Phe | Thr | Met | Pro | Val | Arg | Thr | Ala | Lys | Ser | Leu | Val | Thr | Val | Leu | Gly | 115 | 120 | 125 |     |
| Ile | Pro | Gln | Lys | Pro | Ile | Ile | Thr | Gly | Tyr | Lys | Ser | Ser | Leu | Arg | Glu | 130 | 135 | 140 |     |
| Lys | Asp | Thr | Ala | Thr | Leu | Asn | Cys | Gln | Ser | Ser | Gly | Ser | Lys | Pro | Ala | 145 | 150 | 155 | 160 |
| Ala | Arg | Leu | Thr | Trp | Arg | Lys | Gly | Asp | Gln | Glu | Leu | His | Gly | Glu | Pro | 165 | 170 | 175 |     |
| Thr | Arg | Ile | Gln | Glu | Asp | Pro | Asn | Gly | Lys | Thr | Phe | Thr | Val | Ser | Ser | 180 | 185 | 190 |     |
| Ser | Val | Thr | Phe | Gln | Val | Thr | Arg | Glu | Asp | Asp | Gly | Ala | Ser | Ile | Val | 195 | 200 | 205 |     |
| Cys | Ser | Val | Asn | His | Glu | Ser | Leu | Lys | Gly | Ala | Asp | Arg | Ser | Thr | Ser | 210 | 215 | 220 |     |
| Gln | Arg | Ile | Glu | Val | Leu | Tyr | Thr | Pro | Thr | Ala | Met | Ile | Arg | Pro | Asp | 225 | 230 | 235 | 240 |
| Pro | Pro | His | Pro | Arg | Glu | Gly | Gln | Lys | Leu | Leu | Leu | His | Cys | Glu | Gly | 245 | 250 | 255 |     |
| Arg | Gly | Asn | Pro | Val | Pro | Gln | Gln | Tyr | Leu | Trp | Glu | Lys | Glu | Gly | Ser | 260 | 265 | 270 |     |
| Val | Pro | Pro | Leu | Lys | Met | Thr | Gln | Glu | Ser | Ala | Leu | Ile | Phe | Pro | Phe | 275 | 280 | 285 |     |

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Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

0905348-01301



## oligonucleotide probe

<400> 87  
 cctagcacag tgacgaggga cttggc 26

<210> 88  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 88  
 aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 89  
 gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90  
 <211> 2755  
 <212> DNA  
 <213> Homo sapiens

<400> 90  
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<210> 91
<211> 696
<212> PRT
<213> Homo sapiens

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Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
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Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
 85 90 95

```

|     |     |     |            |            |            |     |     |     |     |            |            |     |     |     |            |
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| Ile | Asn | Asn | Asn<br>115 | Lys        | Ile        | Lys | Ser | Phe | Arg | Lys        | Gln        | Thr | Phe | Leu | Gly        |
| Leu | Asp | Asp | Leu        | Glu        | Tyr        | Leu | Gln | Ala | Asp | Phe        | Asn        | Leu | Leu | Arg | Asp        |
| Ile | Asp | Pro | Gly        | Ala        | Phe<br>150 | Gln | Asp | Leu | Asn | Lys<br>155 | Leu        | Glu | Val | Leu | Ile<br>160 |
| Leu | Asn | Asp | Asn        | Leu<br>165 | Ile        | Ser | Thr | Leu | Pro | Ala        | Asn        | Val | Phe | Gln | Tyr<br>175 |
| Val | Pro | Ile | Thr<br>180 | His        | Leu        | Asp | Leu | Arg | Gly | Asn        | Arg        | Leu | Lys | Thr | Leu        |
| Pro | Tyr | Glu | Glu        | Val        | Leu        | Glu | Gln | Ile | Pro | Gly        | Ile        | Ala | Glu | Ile | Leu        |
| Leu | Glu | Asp | Asn        | Pro        | Trp        | Asp | Cys | Thr | Cys | Asp        | Leu        | Leu | Ser | Leu | Lys        |
| Glu | Trp | Leu | Glu        | Asn        | Ile<br>230 | Pro | Lys | Asn | Ala | Leu<br>235 | Ile        | Gly | Arg | Val | Val<br>240 |
| Cys | Glu | Ala | Pro        | Thr<br>245 | Arg        | Leu | Gln | Gly | Lys | Asp        | Leu        | Asn | Glu | Thr | Thr<br>255 |
| Glu | Gln | Asp | Leu        | Cys        | Pro        | Leu | Lys | Asn | Arg | Val        | Asp        | Ser | Ser | Leu | Pro        |
| Ala | Pro | Pro | Ala        | Gln        | Glu        | Glu | Thr | Phe | Ala | Pro        | Gly        | Pro | Leu | Pro | Thr        |
| Pro | Phe | Lys | Thr        | Asn        | Gly        | Gln | Glu | Asp | His | Ala        | Thr<br>300 | Pro | Gly | Ser | Ala        |
| Pro | Asn | Gly | Gly        | Thr<br>310 | Lys        | Ile | Pro | Gly | Asn | Trp        | Gln        | Ile | Lys | Ile | Arg<br>320 |
| Pro | Thr | Ala | Ala        | Ile<br>325 | Ala        | Thr | Gly | Ser | Ser | Arg        | Asn        | Lys | Pro | Leu | Ala<br>335 |
| Asn | Ser | Leu | Pro        | Cys        | Pro        | Gly | Gly | Cys | Ser | Cys        | Asp        | His | Ile | Pro | Gly        |
| Ser | Gly | Leu | Lys        | Met        | Asn        | Cys | Asn | Asn | Arg | Asn        | Val        | Ser | Ser | Leu | Ala        |
| Asp | Leu | Lys | Pro        | Lys        | Leu        | Ser | Asn | Val | Gln | Glu        | Leu        | Phe | Leu | Arg | Asp        |

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

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|                                                                    |     |     |     |    |
|--------------------------------------------------------------------|-----|-----|-----|----|
|                                                                    | 660 | 665 | 670 |    |
| Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp    |     |     |     |    |
|                                                                    | 675 | 680 | 685 |    |
| Cys Gly Ser His Ser Leu Ser Asp                                    |     |     |     |    |
|                                                                    | 690 | 695 |     |    |
| <210> 92                                                           |     |     |     |    |
| <211> 22                                                           |     |     |     |    |
| <212> DNA                                                          |     |     |     |    |
| <213> Artificial Sequence                                          |     |     |     |    |
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| <223> Description of Artificial Sequence: Synthetic                |     |     |     |    |
| oligonucleotide probe                                              |     |     |     |    |
| <400> 92                                                           |     |     |     |    |
| gttggatctg ggcaacaata ac                                           |     |     |     | 22 |
| <210> 93                                                           |     |     |     |    |
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| oligonucleotide probe                                              |     |     |     |    |
| <400> 93                                                           |     |     |     |    |
| attgttgtgc aggctgagtt taag                                         |     |     |     | 24 |
| <210> 94                                                           |     |     |     |    |
| <211> 45                                                           |     |     |     |    |
| <212> DNA                                                          |     |     |     |    |
| <213> Artificial Sequence                                          |     |     |     |    |
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| oligonucleotide probe                                              |     |     |     |    |
| <400> 94                                                           |     |     |     |    |
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| <210> 95                                                           |     |     |     |    |
| <211> 2226                                                         |     |     |     |    |
| <212> DNA                                                          |     |     |     |    |
| <213> Homo sapiens                                                 |     |     |     |    |
| <400> 95                                                           |     |     |     |    |
| agtcgactgc gtcccctgta cccggcgcca gctgtgttcc tgaccccaga ataactcagg  | 60  |     |     |    |
| gctgcaccgg gcttggcagc gctccgcaca catttcctgt cgcggcctaa gggaaactgt  | 120 |     |     |    |
| tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgctcggg agcgagggcg | 180 |     |     |    |

gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240  
 ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300  
 ggggcctcag agaatgaggc cggcgttcgc cctgtgcctc ctctggcagg cgctctggcc 360  
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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

TOEFL-20-24E50650

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Gly | Ala | Glu | Leu | Arg | Ala | Val | Leu | Ala | Leu | Leu | Arg | Ala | Gly | 65  | 70  | 75  | 80  |
| Pro | Gly | Pro | Gly | Gly | Gly | Ser | Lys | Asp | Leu | Leu | Phe | Trp | Val | Ala | Leu | 85  | 90  | 95  |     |
| Glu | Arg | Arg | Arg | Ser | His | Cys | Thr | Leu | Glu | Asn | Glu | Pro | Leu | Arg | Gly | 100 | 105 | 110 |     |
| Phe | Ser | Trp | Leu | Ser | Ser | Asp | Pro | Gly | Gly | Leu | Glu | Ser | Asp | Thr | Leu | 115 | 120 | 125 |     |
| Gln | Trp | Val | Glu | Glu | Pro | Gln | Arg | Ser | Cys | Thr | Ala | Arg | Arg | Cys | Ala | 130 | 135 | 140 |     |
| Val | Leu | Gln | Ala | Thr | Gly | Gly | Val | Glu | Pro | Ala | Gly | Trp | Lys | Glu | Met | 145 | 150 | 155 | 160 |
| Arg | Cys | His | Leu | Arg | Ala | Asn | Gly | Tyr | Leu | Cys | Lys | Tyr | Gln | Phe | Glu | 165 | 170 | 175 |     |
| Val | Leu | Cys | Pro | Ala | Pro | Arg | Pro | Gly | Ala | Ala | Ser | Asn | Leu | Ser | Tyr | 180 | 185 | 190 |     |
| Arg | Ala | Pro | Phe | Gln | Leu | His | Ser | Ala | Ala | Leu | Asp | Phe | Ser | Pro | Pro | 195 | 200 | 205 |     |
| Gly | Thr | Glu | Val | Ser | Ala | Leu | Cys | Arg | Gly | Gln | Leu | Pro | Ile | Ser | Val | 210 | 215 | 220 |     |
| Thr | Cys | Ile | Ala | Asp | Glu | Ile | Gly | Ala | Arg | Trp | Asp | Lys | Leu | Ser | Gly | 225 | 230 | 235 | 240 |
| Asp | Val | Leu | Cys | Pro | Cys | Pro | Gly | Arg | Tyr | Leu | Arg | Ala | Gly | Lys | Cys | 245 | 250 | 255 |     |
| Ala | Glu | Leu | Pro | Asn | Cys | Leu | Asp | Asp | Leu | Gly | Gly | Phe | Ala | Cys | Glu | 260 | 265 | 270 |     |
| Cys | Ala | Thr | Gly | Phe | Glu | Leu | Gly | Lys | Asp | Gly | Arg | Ser | Cys | Val | Thr | 275 | 280 | 285 |     |
| Ser | Gly | Glu | Gly | Gln | Pro | Thr | Leu | Gly | Gly | Thr | Gly | Val | Pro | Thr | Arg | 290 | 295 | 300 |     |
| Arg | Pro | Pro | Ala | Thr | Ala | Thr | Ser | Pro | Val | Pro | Gln | Arg | Thr | Trp | Pro | 305 | 310 | 315 | 320 |
| Ile | Arg | Val | Asp | Glu | Lys | Leu | Gly | Glu | Thr | Pro | Leu | Val | Pro | Glu | Gln | 325 | 330 | 335 |     |
| Asp | Asn | Ser | Val | Thr | Ser | Ile | Pro | Glu | Ile | Pro | Arg | Trp | Gly | Ser | Gln |     |     |     |     |

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<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 97
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<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 98
tgaccagtgg ggaaggacag
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20



<210> 99  
 <211> 20  
 <212> DNA  
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 <210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

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<400> 103  
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 ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560  
 actgtgtcca ttttaagctgt attctgccat tgcctttgaa agatctatgt tctctcagta 1620  
 gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680  
 ttgactcttc acatgatgga ggtatgaggg ctccgagata gctgagggaa gttctttgcc 1740  
 tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800  
 ctaaaagtgt caagcgttga cagcttgga gcggtttatt atacatctct gtaaaaggat 1860  
 attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920  
 gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980  
 tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

<210> 104  
 <211> 415  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
 Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala  
 1 5 10 15  
 Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr  
 20 25 30  
 Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly  
 35 40 45  
 Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr  
 50 55 60

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Glu | Gly | Lys | Val | Val | Val | Leu | Asn | Phe | Arg | Phe | Ile | Asp | Leu | 65  | 70  | 75  | 80  |
| Glu | Ser | Asp | Asn | Leu | Cys | Arg | Tyr | Asp | Phe | Val | Asp | Val | Tyr | Asn | Gly | 85  | 90  | 95  |     |
| His | Ala | Asn | Gly | Gln | Arg | Ile | Gly | Arg | Phe | Cys | Gly | Thr | Phe | Arg | Pro | 100 | 105 | 110 |     |
| Gly | Ala | Leu | Val | Ser | Ser | Gly | Asn | Lys | Met | Met | Val | Gln | Met | Ile | Ser | 115 | 120 | 125 |     |
| Asp | Ala | Asn | Thr | Ala | Gly | Asn | Gly | Phe | Met | Ala | Met | Phe | Ser | Ala | Ala | 130 | 135 | 140 |     |
| Glu | Pro | Asn | Glu | Arg | Gly | Asp | Gln | Tyr | Cys | Gly | Gly | Leu | Leu | Asp | Arg | 145 | 150 | 155 | 160 |
| Pro | Ser | Gly | Ser | Phe | Lys | Thr | Pro | Asn | Trp | Pro | Asp | Arg | Asp | Tyr | Pro | 165 | 170 | 175 |     |
| Ala | Gly | Val | Thr | Cys | Val | Trp | His | Ile | Val | Ala | Pro | Lys | Asn | Gln | Leu | 180 | 185 | 190 |     |
| Ile | Glu | Leu | Lys | Phe | Glu | Lys | Phe | Asp | Val | Glu | Arg | Asp | Asn | Tyr | Cys | 195 | 200 | 205 |     |
| Arg | Tyr | Asp | Tyr | Val | Ala | Val | Phe | Asn | Gly | Gly | Glu | Val | Asn | Asp | Ala | 210 | 215 | 220 |     |
| Arg | Arg | Ile | Gly | Lys | Tyr | Cys | Gly | Asp | Ser | Pro | Pro | Ala | Pro | Ile | Val | 225 | 230 | 235 | 240 |
| Ser | Glu | Arg | Asn | Glu | Leu | Leu | Ile | Gln | Phe | Leu | Ser | Asp | Leu | Ser | Leu | 245 | 250 | 255 |     |
| Thr | Ala | Asp | Gly | Phe | Ile | Gly | His | Tyr | Ile | Phe | Arg | Pro | Lys | Lys | Leu | 260 | 265 | 270 |     |
| Pro | Thr | Thr | Thr | Glu | Gln | Pro | Val | Thr | Thr | Thr | Phe | Pro | Val | Thr | Thr | 275 | 280 | 285 |     |
| Gly | Leu | Lys | Pro | Thr | Val | Ala | Leu | Cys | Gln | Gln | Lys | Cys | Arg | Arg | Thr | 290 | 295 | 300 |     |
| Gly | Thr | Leu | Glu | Gly | Asn | Tyr | Cys | Ser | Ser | Asp | Phe | Val | Leu | Ala | Gly | 305 | 310 | 315 | 320 |
| Thr | Val | Ile | Thr | Thr | Ile | Thr | Arg | Asp | Gly | Ser | Leu | His | Ala | Thr | Val | 325 | 330 | 335 |     |
| Ser | Ile | Ile | Asn | Ile | Tyr | Lys | Glu | Gly | Asn | Leu | Ala | Ile | Gln | Gln | Ala |     |     |     |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 340 |     | 345 |     | 350 |     |     |     |     |     |     |     |     |     |     |
| Gly | Lys | Asn | Met | Ser | Ala | Arg | Leu | Thr | Val | Val | Cys | Lys | Gln | Cys | Pro |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Leu | Arg | Arg | Gly | Leu | Asn | Tyr | Ile | Ile | Met | Gly | Gln | Val | Gly | Glu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asp | Gly | Arg | Gly | Lys | Ile | Met | Pro | Asn | Ser | Phe | Ile | Met | Met | Phe | Lys |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Thr | Lys | Asn | Gln | Lys | Leu | Leu | Asp | Ala | Leu | Lys | Asn | Lys | Gln | Cys |     |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

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<213> Homo sapiens

<400> 108

cggacgcgtg ggccggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60  
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 aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct ccaggacct 180  
 atctggctcc agccctctcc acctccccag tcttctcccc cgctcagcc ccatccgtgt 240  
 catacctgcc ggggactggg tgacagcttt aacaagggcc tggagagaac catccggggac 300  
 aactttggag gtggaaacac tgccctgggag gaagagaatt tgtccaaata caaagacagt 360  
 gagaccgcgc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420  
 cgctgctgg agctgagtga ggagctgggt gagagctggg ggtttcacaa gcagcaggag 480  
 gccccggacc tcttccagtg gctgtgctca gattccctga agctctgctg ccccgaggc 540  
 accttcgggc cctcctgcct tccctgtcct gggggaacag agaggccctg cgggtggctac 600  
 gggcagtgtg aaggagaagg gacacgaggg ggacgcgggc actgtgactg ccaagccggc 660  
 tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720  
 agccatctgg tatgttcggc ttgttttggc ccctgtgccc gatgctcagg acctgaggaa 780  
 tcaaaactgt tgcaatgcaa gaagggtgtg gccctgcctc acctcaagtg tgtagacatt 840  
 gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900  
 ggctcctatg agtgccgaga ctgtgccaaag gcctgcctag gctgcatggg ggcaggggca 960  
 ggtcgctgta agaagtgtag ccctggctat cagcagggtg gctccaagtg tctcgatgtg 1020  
 gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080  
 ggttatcgct gcatctgtgc cgagggtac aagcagatgg aaggcatctg tgtgaaggag 1140  
 cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200  
 cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taaggcgac 1260  
 ttggtgttca ccgccatctt cattgggggt gtggcgcca tgactggcta ctggttgtca 1320  
 gagegcagtg accgtgtgct ggagggtctt atcaaggcca gataatcgcg gccaccacct 1380  
 gtaggacctc ctcccacca cgctgcccc agagcttggg ctgccctcct gctggacact 1440  
 caggacagct tgggttattt ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500  
 gccagggtac ccaggcccgg gcagacaagg cccctgggtg aaaaagtagc cctgaagggtg 1560  
 gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620  
 agtttttctt taatggtggc tgctagagct ttggccctg cttaggatta ggtggtcctc 1680  
 acagggtgtg ggccatcaca gctccctcct gccagctgca tgctgccagt tcctgttctg 1740  
 tgttcaccac atccccacac cccattgcca cttatttatt catctcagga aataaagaaa 1800  
 ggtcttgtaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly  
 1 5 10 15  
 Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser  
 20 25 30  
 Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr  
 35 40 45  
 Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile  
 50 55 60

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Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

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Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405 410 415

Ile Lys Gly Arg  
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

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<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgcctcttgc tccctccaggg 60  
 cagcaccatg cagccccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120  
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcaccccca cccacgtgag 240  
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300  
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctggtgttc ggcattggagc agcggctgcc gcccaacagc gagctggtgc aggcctgct 420  
 gcggctcttc caggagccgg tccccaaagg ccgcgtgcac aggcacgggc ggctgtcccc 480  
 gcgcagcgcc cggggccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
 ccgcacctcc ctcatcgact ccaggctggg gtccgtccac gagagcggct ggaaggcctt 600  
 cgacgtgacc gaggcctga acttctggca gcagctgagc cggccccggc agccgctgct 660  
 gctacaggtg tcggtgcaga gggagcatct gggcccgctg gcgtccggcg cccacaagct 720  
 ggtecgcttt gectcgagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gacctgaag caccaatgac 840  
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900  
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960  
 gcagcccccg gaggccttg ccttcaagtg gccgtttctg gggcctcgac agtgcacgc 1020  
 ctcgagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080  
 ccaggtggtc agcctgccc acatgagggt gcagaagtgc agctgtgcct cggatgggtgc 1140  
 gctcgtgcca aggaggtcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
 gtgtgtgttt ctgaagtgt cgaggggtacc aggagagctg gcgatgactg aactgctgat 1260  
 ggacaaatgc tctgtgctct ctagtgagcc ctgaatttgc ttctctgac aagttacctc 1320  
 acctaatatt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380  
 ttctctatcc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440  
 acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
 aaagtccctc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45

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Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

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 08E50660

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
355 360 365

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

```
<210> 116
<211> 22
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

```
<400> 116
ataggagttg aagcagcgcct qc 22
```

```
<210> 117
<211> 45
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 117  
tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

```
<210> 118
<211> 1857
<212> DNA
<213> Homo sapiens
```

```
<400> 118
gtctgttccc aggagtcctt cggcggtctg tgtgtcagtg gcttgatcgc gatggggaca 60
aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
ctggcatttg qcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180
```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240  
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300  
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acggggaagac 360  
actgggacat acacttgat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420  
gtcaagctca tegtgttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480  
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540  
tacacctggt tcaaagatgg gatagtgat cctacgaatc ccaaaagcac ccgtgccttc 600  
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccccgtca 660  
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720  
tcaaatgctg tgcgcagtga agctgtggag cggaatgtgg gggatcatcg ggcagccgtc 780  
cttghtaacc tgattctcct gggaatcttg gtttttggca tctgggttgc ctatagccga 840  
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900  
agtggccgaa gtgaaggaga attcaaacag acctcgatcat tctgggtgtg agcctgggtc 960  
gctcaccgcc tatcatctgc atttgcctta ctccaggtgct accggactct ggccccctgat 1020  
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc ccctacttct 1080  
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tcttccatgc cctccctccc 1140  
tttctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200  
agggatcagg aaggaatcct gggtatgccca ttgacttccc ttctaagtag acagcaaaaa 1260  
tggcgggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320  
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tccttccatc tctggggccc actctcttct gtcttcccat gggaagtgcc actggggatcc 1500  
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accgtgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680  
cagaggctga ggcagggcga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740  
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtgcatgc ctgtagtccc 1800  
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95

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Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
                   100                  105                  110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
                   115                  120                  125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
                   130                  135                  140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145                  150                  155                  160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
                   165                  170                  175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
                   180                  185                  190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
                   195                  200                  205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
                   210                  215                  220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225                  230                  235                  240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
                   245                  250                  255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
                   260                  265                  270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
                   275                  280                  285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
                   290                  295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

0905348 "071301

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctgggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

090548-01301  
 TOTAL 20-84E90660

## oligonucleotide probe

&lt;400&gt; 125

actcagcagtg ggtaggaaag

20

&lt;210&gt; 126

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

cagcgcgtgg ccggcgccgc tgtgggggaca gcatgagcgg cggttggatg gcgcaggttg 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctccggactag 120  
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300  
ggattgagcc atgtacccag aaagggcaat gccaccgcc ccctggcctc ccctgcccct 360  
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgtgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540  
atgagatcct ccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600  
tcacctctct caggaatgcc acaaccatgg ggccccctgt gacctggag agtgtccccct 660  
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720  
gggttattgc agctgctgcg gtgctcagtg caagcctggc caccgccacc ctccctcttt 780  
tgtcctggct ccgagcccag gaggcctcc gccactggg gttactggtg gccatgaagg 840  
agtccttgcct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900  
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaaccgcagc 1020  
tcctgcagaa gtggccctgg agattgaggg tccttgagca ctccctatgg agatccgggg 1080  
agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200  
aagttgcttc 1210

&lt;210&gt; 127

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

0905348-0101

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                                     85                                    90                                    95  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                                     100                                    105                                    110  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                                     115                                    120                                    125  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                                     130                                    135                                    140  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                                     145                                    150                                    155                                    160  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                                     165                                    170                                    175  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                                     180                                    185                                    190  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                                     195                                    200                                    205  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                                     210                                    215                                    220  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala  
                                     225                                    230                                    235                                    240  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                                     245                                    250                                    255  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                                     260                                    265                                    270  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                                     275                                    280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cgggtctcgct cgctcgcgca gcggcgccag cagaggctgc gcacagatgc 60  
 ggggttagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagaccca 120  
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccoga 180  
 gcaatggaga tggatttcta gaggcagcag agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatectg tggtttcagc tggcgctgtg ctteggccct gcacagctca 300  
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg g cattcccgag aatggcttca 360  
 ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactg 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600  
 atgaaggatt caagatccgg taccgccgacc tacacaatat ggtttcatta tgtcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780  
 atcgctgctt tcccgatttt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840  
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cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200  
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 taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740  
 ctgatcctta aaattgctat gctgatagag tggtagaggc tggaagcttg atcaagtcct 1800  
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
 1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

090548-07301

|                                                                 |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|
|                                                                 | 180 |     | 185 |     | 190 |
| Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr | 195 | 200 | 205 |     |     |
| Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys | 210 | 215 | 220 |     |     |
| Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu | 225 | 230 | 235 | 240 |     |
| Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe | 245 | 250 | 255 |     |     |
| Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val | 260 | 265 | 270 |     |     |
| Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr | 275 | 280 | 285 |     |     |
| Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys | 290 | 295 | 300 |     |     |
| Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr | 305 | 310 | 315 | 320 |     |
| Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu | 325 | 330 | 335 |     |     |
| Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His | 340 | 345 | 350 |     |     |
| Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe | 355 | 360 | 365 |     |     |
| Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala | 370 | 375 | 380 |     |     |
| Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val | 385 | 390 | 395 | 400 |     |
| Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr | 405 | 410 | 415 |     |     |
| Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys | 420 | 425 | 430 |     |     |
| Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro | 435 | 440 | 445 |     |     |
| Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile | 450 | 455 | 460 |     |     |

090534-01301  
 TDE720-BHE0660

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gctcccgctg cggcccgctc gtggcctaga 60  
gatgctgctg ccgcggttgc agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120  
ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240  
tgagtgcctc ggatttgac ctacaggag ggcagccagt ctgccgggga gggacacaga 300

09905348-01301

```

ggccttggtta taaagtcatt tacttccatg atactttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtcct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
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gcgaggctcg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggccccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
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gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccct ctcctcctcc 900
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tccagctcga ccttatgaga aggtaccttg ccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tgggtgggtt tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

```

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
 1 5 10 15

```

```

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
 20 25 30

```

```

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
 35 40 45

```

```

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
 50 55 60

```

```

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
 65 70 75 80

```

```

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
 85 90 95

```

```

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
 100 105 110

```

FOR "20" 8450550

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

&lt;210&gt; 138

TOE T 20 " 84E50660

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaaggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 gcatccgcag gttcccgcgg acttgggggc gccgctgag ccccgccgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccgcg agggcagcga gggcctacca ccattgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgactctg 240  
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 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360  
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 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggct cgaaaccata 480  
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 tgtggaagac attcccttcc ttccaccaac cttcaaccca caggaggtct ttattcgctc 660  
 cactaacatt ttctcggaatc tggagtcac cggttgtttg ctggctgggc ttttccagtg 720

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780  
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 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
 gaccctgggg atttttgacc acaaatggcc acggtttgct gttgacctga ccatggaact 1260  
 ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320  
 ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380  
 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaacctc aggtgatgga 1440  
 agttggaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500  
 gcctttatac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val  
 1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala  
 20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu  
 35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro  
 50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu  
 65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu  
 85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu  
 100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly  
 115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val  
 130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe  
 145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu  
 165 170 175

09905348-071301

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

0905348-071301  
 105720-8450660



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac ctacacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

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gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
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atctaattag atataaaatt ctggttaact tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

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<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

TEXT-20" BHE50550

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

0905348-074301

## oligonucleotide probe

&lt;400&gt; 149

ttcagctcat caccttcacc tgcc

24

&lt;210&gt; 150

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 150

ggctcataca aaataccact aggg

24

&lt;210&gt; 151

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

&lt;210&gt; 152

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctgacactcg 60  
 acccacgcgt ccgcggacgc gtgggcggac gcgtgggccc gctaccagga agagtctgcc 120  
 gaaggatgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180  
 cctgggcgtc ttccggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240  
 gaatgctgtg gtggtgatca caggcgccac ctgaggctg ggcaaagaat gtgcaaaagt 300  
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 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
 ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480  
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 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600  
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 catcagcagc atccagggca agatgagcat tccttttcca tcagcatatg cagcctccaa 720  
 gcacgcaacc caggctttct ttgactgtct gcgtgcccag atggaacagt atgaaattga 780  
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 ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960  
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090548-07301

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 gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc caggggtgagg 1260  
 ggaaacactt aaggaataaa tatggagctg ggggtttaaca ctaaaaacta gaaataaaca 1320  
 tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380  
 cttggccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
 1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
 20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly  
 35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala  
 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
 195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
 225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
 245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val  
 260 265 270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
 275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
 290 295 300

Arg Lys Ser Lys Asn Ser  
 305 310

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 154  
 ggtgctaaac tgggtgctctg tggc 24

<210> 155  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 155  
 cagggcaaga tgagcattcc 20

<210> 156  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

090548-01E50660

<400> 156  
tcatactgtt ccatctcggc acgc

24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcacgc cttctcatgc

50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacacccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
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tataaataag catggactgg aggaaacagc tgccaaatgc aagggaactgg gtgccaaggt 360  
tcataccttt gtggttagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggtgtg tctatacatc 480  
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
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aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaaaca catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780  
aaatccaagt acaagtttg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

090549-01301

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val  
 1 5 10 15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
 20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
 35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
 50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
 65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
 85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
 100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
 115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
 130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr  
 145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
 165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
 195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
 210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
 225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
 245 250 255

090548-07101  
 FEB 20 8 45 AM '66



Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 161

atcccatgca tcagcctggt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

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 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

0905348-0101

attgtttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180  
 agaagtgttt ccatgccacc taagggagac tcaggacagc cattatctct cacccttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggctcgccc tttcccagga 300  
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360  
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 ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
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 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
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 ataatagttt tggggaaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

090543 07131

|                                                                 |     |    |     |    |     |     |
|-----------------------------------------------------------------|-----|----|-----|----|-----|-----|
| 65                                                              |     | 70 |     | 75 |     | 80  |
| Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln | 85  |    | 90  |    | 95  |     |
| Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro | 100 |    | 105 |    | 110 |     |
| Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val | 115 |    | 120 |    | 125 |     |
| Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr | 130 |    | 135 |    | 140 |     |
| Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser | 145 |    | 150 |    | 155 | 160 |
| Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala | 165 |    | 170 |    | 175 |     |
| Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu | 180 |    | 185 |    | 190 |     |
| Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys | 195 |    | 200 |    | 205 |     |
| Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg | 210 |    | 215 |    | 220 |     |
| Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser | 225 |    | 230 |    | 235 | 240 |
| Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile | 245 |    | 250 |    | 255 |     |
| Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His | 260 |    | 265 |    | 270 |     |
| Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu | 275 |    | 280 |    | 285 |     |
| Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr | 290 |    | 295 |    | 300 |     |
| Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys | 305 |    | 310 |    | 315 | 320 |
| Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro | 325 |    | 330 |    | 335 |     |
| Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly | 340 |    | 345 |    | 350 |     |

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Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165

ttccatgcca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

0905348.01301

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

agctctcaqa ggctggtcat aggg

24

<211> 50

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<211> 2477

<212> DNA

<213> Homo sapiens

|             |             |            |             |             |             |      |
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| cagagggcttt | tccggctccg  | gaatggcaca | tgtgggaatc  | ccagtcttgt  | tggctacaac  | 60   |
| atTTTTccct  | ttcctaacaa  | gttctaacag | ctgttctaac  | agctagtgat  | caggggttct  | 120  |
| tcttgctgga  | gaagaaagg   | ctgagggcag | agcagggcac  | tctcactcag  | ggtgaccagc  | 180  |
| tccttgcttc  | tctgtggata  | acagagcatg | agaaagtga   | gagatgcagc  | ggagtgaggt  | 240  |
| gatggaagtc  | taaaatagga  | aggaatTTTg | tgtgcaatat  | cagactctgg  | gagcagttga  | 300  |
| cctggagagc  | ctgggggagg  | gcctgcctaa | caagctttca  | aaaaacagga  | gcgacttcca  | 360  |
| ctgggctggg  | ataagacgtg  | ccggtaggat | aggggaagact | gggtttagtc  | ctaatatcaa  | 420  |
| attgactggc  | tgggtgaact  | tcaacagcct | tttaacctct  | ctgggagatg  | aaaacgatgg  | 480  |
| cttaaggggc  | cagaaataga  | gatgctttgt | aaaataaaat  | tttaaaaaaa  | gcaagtattt  | 540  |
| tatagcataa  | aggctagaga  | ccaaaataga | taacaggatt  | ccctgaacat  | tctaagagag  | 600  |
| gagaaagtat  | gttaaaaata  | gaaaacccaa | aatgcagaag  | gaggagactc  | acagagctaa  | 660  |
| accaggatgg  | ggaccctggg  | tacggccagc | ctctttgtct  | ctcccggaaa  | ttatTTTTgg  | 720  |
| tctgaccaact | ctgccttgtg  | ttttgcbaga | tcatgtgagg  | gccaaaccggg | gaaggtggag  | 780  |
| cagatgagca  | cacacaggag  | ccgtctcctc | accgcgcgcc  | ctctcagcat  | ggaacagagg  | 840  |
| cagccctggc  | cccgggccct  | ggaggtggac | agccgtctct  | tggctcctgt  | ctcagtggtc  | 900  |
| tgggtgctgc  | tggccccccc  | agcagccggc | atgcctcagt  | tcagcacctt  | ccactctgag  | 960  |
| aatcgtgact  | ggaccttcaa  | ccacttgacc | gtccaccaag  | ggacgggggc  | cgtctatgtg  | 1020 |
| ggggccatca  | accgggtcta  | taagctgaca | ggcaacctga  | ccatccaggt  | ggctcataag  | 1080 |
| acagggccag  | aagaggacaa  | caagtctcgt | taccgccccc  | tcatcgtgca  | gccttgccagc | 1140 |
| gaagtgtcca  | ccctcaccaa  | caatgtcaac | aagctgctca  | tcattgacta  | ctctgagaac  | 1200 |
| cgctgctgg   | cctgtgggag  | cctctaccag | ggggctctgca | agctgctgcg  | gctggatgac  | 1260 |
| ctcttcatcc  | tgggtggagcc | atcccacaag | aaggagcact  | acctgtccag  | tgtcaacaag  | 1320 |
| acgggcacca  | tgtacggggg  | gattgtgcgc | tctgaggggt  | aggatggcaa  | gctcttcctc  | 1380 |
| ggcacggctg  | tggatgggaa  | gcaggattac | ttcccgaacc  | tgtccagccg  | gaagctggcc  | 1440 |
| cgagaccctg  | agtccctcagc | catgctcgac | tatgagctac  | acagcgattt  | tgtctcctct  | 1500 |
| ctcatcaaga  | tccttccaga  | caccctggcc | ctggctccc   | actttgacat  | cttctacatc  | 1560 |
| tacggctttg  | ctagtggggg  | ctttgtctac | tttctcactg  | tccagcccga  | gacccctgag  | 1620 |
| ggtgtggcca  | tcaactccgc  | tggagacctc | ttctacacct  | cacgcacgt   | gcggctctgc  | 1680 |

aaggatgacc ccaagttcca ctcatagctg tccctgccct tcggctgcac ccgggccggg 1740  
gtggaataacc gcctcctgca ggctgcttac ctggccaagc ctgggggactc actggcccag 1800  
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860  
cagtatcacc acccgcccgga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920  
ttgcagatca aggagcgctt gcagtcctgc taccagggcg agggcaacct ggagctcaac 1980  
tggctgctgg ggaaggacgt ccagtgcacg aaggcgctg tccccatcga tgataacttc 2040  
tgtggactgg acatcaacca gccctggga ggctcaactc cagtggaggg cctgacctg 2100  
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggctacagc 2160  
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agatttaact ataggcaact ttattttctt ggggaacaaa ggtgaaatgg ggaggtaaga 2340  
aggggttaat tttgtgactt agcttctagc tacttctctc agccatcagt cattgggtat 2400  
gtaaggaatg caagcgattt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460  
acatctgcaa aagcaaa 2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr  
1 5 10 15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly  
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val  
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val  
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser  
165 170 175

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Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

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450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataaccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctccccg gcgcggctga gtgcggactg gagtgggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcg cttgggcttc ctgggtgctcc gcaggctgga ctggagcacc ctgggccctc 180  
tgcggtcccg ccatcgacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactattt ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgctg ccaggccccct 480  
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tgagagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tcctgacttc agacaacaag gatgggctga 780  
gcaaggggat tgtccaggga gtcttgacca ccatcaactt gcagtcaaca cagagctgc 840  
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cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcattctgctg 2340  
 gactcaggcg tgcctcttgc tggttcctgg gaggttggc cacatccctc atggcccat 2400  
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 gaagtgtgtc caagtccgca tttagcctt gttctggggc ccagcccaac acctggcttg 3060  
 ggctcactgt cctgagttgc agtaaagcta taaccttgaa tcacaa 3106

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu  
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Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp  
 20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln  
 35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe  
 50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp  
 65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr  
 85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser  
 100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly  
 115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp  
 130 135 140

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Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

09905348 "071301

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| ggggacgcgg | agctgagagg | ctccggggcta | gctaggtgta | ggggtggacg | ggtcccagga  | 60  |
| ccctggtgag | ggttctctac | ttggcctteg  | gtgggggtca | agacgcaggc | acctacgcca  | 120 |
| aaggggagca | aagccgggct | cggcccagg   | ccccaggac  | ctccatctcc | caatgttggga | 180 |
| ggaatccgac | acgtgacggg | ctgtccgcg   | tctcagacta | gaggagcgct | gtaaacgcca  | 240 |
| tggctcccaa | gaagctgtcc | tgccttcgtt  | ccctgctgct | gccgctcagc | ctgacgctac  | 300 |
| tgctgcccc  | ggcagacact | cggtcgttcg  | tagtggatag | gggtcatgac | cggtttctcc  | 360 |
| tagacggggc | cccgttccgc | tatgtgtctg  | gcagcctgca | ctactttcgg | gtaccgcggg  | 420 |

tgctttgggc cgaccggcctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480  
 atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540  
 acctcattgc ctttctgaat gaggcagctc tagcgaacct gttgggtcata ctgagaccag 600  
 gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660  
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720  
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<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

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Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Leu | Leu | Lys | Met | Arg | Trp | Ser | Gly | Leu | Asn | Ala | Ile | Gln | Phe | 65  | 70  | 75  | 80  |
| Tyr | Val | Pro | Trp | Asn | Tyr | His | Glu | Pro | Gln | Pro | Gly | Val | Tyr | Asn | Phe | 85  | 90  | 95  |     |
| Asn | Gly | Ser | Arg | Asp | Leu | Ile | Ala | Phe | Leu | Asn | Glu | Ala | Ala | Leu | Ala | 100 | 105 | 110 |     |
| Asn | Leu | Leu | Val | Ile | Leu | Arg | Pro | Gly | Pro | Tyr | Ile | Cys | Ala | Glu | Trp | 115 | 120 | 125 |     |
| Glu | Met | Gly | Gly | Leu | Pro | Ser | Trp | Leu | Leu | Arg | Lys | Pro | Glu | Ile | His | 130 | 135 | 140 |     |
| Leu | Arg | Thr | Ser | Asp | Pro | Asp | Phe | Leu | Ala | Ala | Val | Asp | Ser | Trp | Phe | 145 | 150 | 155 | 160 |
| Lys | Val | Leu | Leu | Pro | Lys | Ile | Tyr | Pro | Trp | Leu | Tyr | His | Asn | Gly | Gly | 165 | 170 | 175 |     |
| Asn | Ile | Ile | Ser | Ile | Gln | Val | Glu | Asn | Glu | Tyr | Gly | Ser | Tyr | Arg | Ala | 180 | 185 | 190 |     |
| Cys | Asp | Phe | Ser | Tyr | Met | Arg | His | Leu | Ala | Gly | Leu | Phe | Arg | Ala | Leu | 195 | 200 | 205 |     |
| Leu | Gly | Glu | Lys | Ile | Leu | Leu | Phe | Thr | Thr | Asp | Gly | Pro | Glu | Gly | Leu | 210 | 215 | 220 |     |
| Lys | Cys | Gly | Ser | Leu | Arg | Gly | Leu | Tyr | Thr | Thr | Val | Asp | Phe | Gly | Pro | 225 | 230 | 235 | 240 |
| Ala | Asp | Asn | Met | Thr | Lys | Ile | Phe | Thr | Leu | Leu | Arg | Lys | Tyr | Glu | Pro | 245 | 250 | 255 |     |
| His | Gly | Pro | Leu | Val | Asn | Ser | Glu | Tyr | Tyr | Thr | Gly | Trp | Leu | Asp | Tyr | 260 | 265 | 270 |     |
| Trp | Gly | Gln | Asn | His | Ser | Thr | Arg | Ser | Val | Ser | Ala | Val | Thr | Lys | Gly | 275 | 280 | 285 |     |
| Leu | Glu | Asn | Met | Leu | Lys | Leu | Gly | Ala | Ser | Val | Asn | Met | Tyr | Met | Phe | 290 | 295 | 300 |     |
| His | Gly | Gly | Thr | Asn | Phe | Gly | Tyr | Trp | Asn | Gly | Ala | Asp | Lys | Lys | Gly | 305 | 310 | 315 | 320 |
| Arg | Phe | Leu | Pro | Ile | Thr | Thr | Ser | Tyr | Asp | Tyr | Asp | Ala | Pro | Ile | Ser | 325 | 330 | 335 |     |
| Glu | Ala | Gly | Asp | Pro | Thr | Pro | Lys | Leu | Phe | Ala | Leu | Arg | Asp | Val | Ile |     |     |     |     |

0905348-07101  
TOT 20" 84E50660

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 340 |     | 345 |     | 350 |     |     |     |     |     |     |     |     |     |     |
| Ser | Lys | Phe | Gln | Glu | Val | Pro | Leu | Gly | Pro | Leu | Pro | Pro | Pro | Ser | Pro |
|     | 355 |     |     |     |     |     | 360 |     |     |     | 365 |     |     |     |     |
| Lys | Met | Met | Leu | Gly | Pro | Val | Thr | Leu | His | Leu | Val | Gly | His | Leu | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Phe | Leu | Asp | Leu | Leu | Cys | Pro | Arg | Gly | Pro | Ile | His | Ser | Ile | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Pro | Met | Thr | Phe | Glu | Ala | Val | Lys | Gln | Asp | His | Gly | Phe | Met | Leu | Tyr |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Arg | Thr | Tyr | Met | Thr | His | Thr | Ile | Phe | Glu | Pro | Thr | Pro | Phe | Trp | Val |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Pro | Asn | Asn | Gly | Val | His | Asp | Arg | Ala | Tyr | Val | Met | Val | Asp | Gly | Val |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Phe | Gln | Gly | Val | Val | Glu | Arg | Asn | Met | Arg | Asp | Lys | Leu | Phe | Leu | Thr |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gly | Lys | Leu | Gly | Ser | Lys | Leu | Asp | Ile | Leu | Val | Glu | Asn | Met | Gly | Arg |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Leu | Ser | Phe | Gly | Ser | Asn | Ser | Ser | Asp | Phe | Lys | Gly | Leu | Leu | Lys | Pro |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Pro | Ile | Leu | Gly | Gln | Thr | Ile | Leu | Thr | Gln | Trp | Met | Met | Phe | Pro | Leu |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Lys | Ile | Asp | Asn | Leu | Val | Lys | Trp | Trp | Phe | Pro | Leu | Gln | Leu | Pro | Lys |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Trp | Pro | Tyr | Pro | Gln | Ala | Pro | Ser | Gly | Pro | Thr | Phe | Tyr | Ser | Lys | Thr |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Phe | Pro | Ile | Leu | Gly | Ser | Val | Gly | Asp | Thr | Phe | Leu | Tyr | Leu | Pro | Gly |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Trp | Thr | Lys | Gly | Gln | Val | Trp | Ile | Asn | Gly | Phe | Asn | Leu | Gly | Arg | Tyr |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Trp | Thr | Lys | Gln | Gly | Pro | Gln | Gln | Thr | Leu | Tyr | Val | Pro | Arg | Phe | Leu |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Leu | Phe | Pro | Arg | Gly | Ala | Leu | Asn | Lys | Ile | Thr | Leu | Leu | Glu | Leu | Glu |
|     | 595 |     |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Asp | Val | Pro | Leu | Gln | Pro | Gln | Val | Gln | Phe | Leu | Asp | Lys | Pro | Ile | Leu |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |

0650348-07130

22



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<220>

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 oligonucleotide probe

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24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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50

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 <212> DNA  
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 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
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 ttggtgtggt cttgtcagaa gttagtgaata ataaacttag ggaaattagt ttgaaccatg 360  
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 tgcactctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
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<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

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Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser  
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Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His  
 50 55 60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe  
 65 70 75 80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His  
 85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln  
 100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala  
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Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro  
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Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu  
 145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser  
 165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val  
 180 185 190

05905348-071301

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 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
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 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
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 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
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 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
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 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
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 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
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&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Val | Arg | Arg | Leu | Met | Pro | Leu | Thr | Leu | Leu | Ile | Leu | Ser | 1   | 5   | 10  | 15  |
| Cys | Leu | Ala | Glu | Leu | Thr | Met | Ala | Glu | Ala | Glu | Gly | Asn | Ala | Ser | Cys | 20  | 25  | 30  |     |
| Thr | Val | Ser | Leu | Gly | Gly | Ala | Asn | Met | Ala | Glu | Thr | His | Lys | Ala | Met | 35  | 40  | 45  |     |
| Ile | Leu | Gln | Leu | Asn | Pro | Ser | Glu | Asn | Cys | Thr | Trp | Thr | Ile | Glu | Arg | 50  | 55  | 60  |     |
| Pro | Glu | Asn | Lys | Ser | Ile | Arg | Ile | Ile | Phe | Ser | Tyr | Val | Gln | Leu | Asp | 65  | 70  | 75  | 80  |
| Pro | Asp | Gly | Ser | Cys | Glu | Ser | Glu | Asn | Ile | Lys | Val | Phe | Asp | Gly | Thr | 85  | 90  | 95  |     |
| Ser | Ser | Asn | Gly | Pro | Leu | Leu | Gly | Gln | Val | Cys | Ser | Lys | Asn | Asp | Tyr | 100 | 105 | 110 |     |
| Val | Pro | Val | Phe | Glu | Ser | Ser | Ser | Ser | Thr | Leu | Thr | Phe | Gln | Ile | Val | 115 | 120 | 125 |     |
| Thr | Asp | Ser | Ala | Arg | Ile | Gln | Arg | Thr | Val | Phe | Val | Phe | Tyr | Tyr | Phe | 130 | 135 | 140 |     |
| Phe | Ser | Pro | Asn | Ile | Ser | Ile | Pro | Asn | Cys | Gly | Gly | Tyr | Leu | Asp | Thr | 145 | 150 | 155 | 160 |
| Leu | Glu | Gly | Ser | Phe | Thr | Ser | Pro | Asn | Tyr | Pro | Lys | Pro | His | Pro | Glu | 165 | 170 | 175 |     |
| Leu | Ala | Tyr | Cys | Val | Trp | His | Ile | Gln | Val | Glu | Lys | Asp | Tyr | Lys | Ile | 180 | 185 | 190 |     |
| Lys | Leu | Asn | Phe | Lys | Glu | Ile | Phe | Leu | Glu | Ile | Asp | Lys | Gln | Cys | Lys | 195 | 200 | 205 |     |
| Phe | Asp | Phe | Leu | Ala | Ile | Tyr | Asp | Gly | Pro | Ser | Thr | Asn | Ser | Gly | Leu | 210 | 215 | 220 |     |
| Ile | Gly | Gln | Val | Cys | Gly | Arg | Val | Thr | Pro | Thr | Phe | Glu | Ser | Ser | Ser | 225 | 230 | 235 | 240 |
| Asn | Ser | Leu | Thr | Val | Val | Leu | Ser | Thr | Asp | Tyr | Ala | Asn | Ser | Tyr | Arg | 245 | 250 | 255 |     |
| Gly | Phe | Ser | Ala | Ser | Tyr | Thr | Ser | Ile | Tyr | Ala | Glu | Asn | Ile | Asn | Thr | 260 | 265 | 270 |     |
| Thr | Ser | Leu | Thr | Cys | Ser | Ser | Asp | Arg | Met | Arg | Val | Ile | Ile | Ser | Lys | 275 | 280 | 285 |     |

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Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

00905348-01304  
 FOOTNOTES

|                                                                           | 565 | 570 | 575 |
|---------------------------------------------------------------------------|-----|-----|-----|
| Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe           | 580 | 585 | 590 |
| Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr               | 595 | 600 | 605 |
| <210> 191                                                                 |     |     |     |
| <211> 21                                                                  |     |     |     |
| <212> DNA                                                                 |     |     |     |
| <213> Artificial Sequence                                                 |     |     |     |
| <220>                                                                     |     |     |     |
| <223> Description of Artificial Sequence: Synthetic oligonucleotide probe |     |     |     |
| <400> 191                                                                 |     |     |     |
| tctctattcc aaactgtggc g                                                   |     |     | 21  |
| <210> 192                                                                 |     |     |     |
| <211> 22                                                                  |     |     |     |
| <212> DNA                                                                 |     |     |     |
| <213> Artificial Sequence                                                 |     |     |     |
| <220>                                                                     |     |     |     |
| <223> Description of Artificial Sequence: Synthetic oligonucleotide probe |     |     |     |
| <400> 192                                                                 |     |     |     |
| tttgatgacg attcgaaggt gg                                                  |     |     | 22  |
| <210> 193                                                                 |     |     |     |
| <211> 47                                                                  |     |     |     |
| <212> DNA                                                                 |     |     |     |
| <213> Artificial Sequence                                                 |     |     |     |
| <220>                                                                     |     |     |     |
| <223> Description of Artificial Sequence: Synthetic oligonucleotide probe |     |     |     |
| <400> 193                                                                 |     |     |     |
| ggaaggatcc ttcaccagcc ccaattaccc aaagccgcac cctgagc                       |     |     | 47  |
| <210> 194                                                                 |     |     |     |
| <211> 2362                                                                |     |     |     |
| <212> DNA                                                                 |     |     |     |
| <213> Homo sapiens                                                        |     |     |     |
| <400> 194                                                                 |     |     |     |
| gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60      |     |     |     |
| cgggacatgc ggccccagga gtcctccagg ctgcgcgttcc cgttgctgct gttgctgttg 120    |     |     |     |
| ctactactac caccgcgcgc gtgcctgcgc cacagcgcca cgcgcttcga cccacctgg 180      |     |     |     |



```

gagtcacctgg acgcccgcga gctgcccgcg tggtttgacc aggccaaagt cggcatcttc 240
atccactggg gagtggtttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360
aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgccaa ccagtgggca 420
gatatttttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccagg 540
agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttggg 600
ctgtactatt ccttttttga atggtttcat ccgctcttcc ttgaggatga atccagtcca 660
ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720
aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780
aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtagtc 840
accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900
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taaactcatt gtgcaaatgt aa 2362

```

&lt;210&gt; 195

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

```

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
 1 5 10 15

```

```

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
 20 25 30

```

```

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
 35 40 45

```

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

TOE 20-84E50550

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
                   340                                  345                                  350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
                   355                                  360                                  365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
                   370                                  375                                  380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
                   385                                  390                                  395                                  400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
                                   405                                  410                                  415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
                   420                                  425                                  430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
                   435                                  440                                  445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
                   450                                  455                                  460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

09905348.071301

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198

aacttgcagc atcagccact ctgc

24

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199

ttccgtgccc agcttcggta gcgagtgggt ctggtgggtat tggca

45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

```

agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60
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catctgaggt gtttccctgg ctctgaaggg gtaggcacga tggccagggt cttcagcctg 180
gtgttgcttc tcaactccat ctggaccacg aggtcctctg tccaaggctc tttgcgtgca 240
gaagagcttt ccatccagggt gtcatgcaga attatgggga tcacccttgt gagcaaaaag 300
gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360
ttggccggga aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
ggctgggttg gagatggatt cgtgggtcatc tctaggatta gcccaaaccc caagtgtggg 480
aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540
tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600
gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660
acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720
ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780
gaaactagca ccatgtctac agaaactgaa ccatttggtg aaaataaagc agcattcaag 840
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tttgggtgctg cagctgggtc tggattttgc tatgtcaaaa ggtatgtgaa ggcttccct 960
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gtcctaataa tatcccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

```

```

tcacagat ccagtggtaa aaaggcctcc tggctgtctg aggctaggtg ggttgaaagc 1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cctttcttca 1560
gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccg taagagcaaa 1620
agaatggcag aaaagtttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
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```

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
 1 5 10 15

```

```

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
 20 25 30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
 35 40 45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
 50 55 60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
 65 70 75 80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
 85 90 95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
 100 105 110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
 115 120 125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
 130 135 140

```

T.D.E.T. 2013450660

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
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 305 310 315 320  
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<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

05905348.071301

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203

gtcagtgaca gtacctactc gg

22

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204

tggagcagga ggagtagtag tagg

24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206

<211> 1620

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (973)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (977)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (996)

<223> a, t, c or g

<220>

<221> modified\_base

0905348-01301  
T0E T20-B4E50650

<222> (1003)

<223> a, t, c or g

<400> 206

```

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ggaaactgcc gccgctctgc caccgtctgc ccaccaacg cgaagacggt aaccctgtg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
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ccaacacaat tcttttcttc cgcttgataa ttgcgatggg cctactttac atcacactct 360
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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

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20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65 70 75 80

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Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
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 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
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 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
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 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
 225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

&lt;210&gt; 208

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 208

gcttgatat tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg

20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg

24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag

50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
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 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

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1

5

10

15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp

20

25

30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys

35

40

45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala

50

55

60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser

65

70

75

80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala

85

90

95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe

100

105

110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

TOE 20" 34E5050

| 115                                                                                | 120 | 125 |
|------------------------------------------------------------------------------------|-----|-----|
| Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr<br>130 135 140     |     |     |
| Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu<br>145 150 155 160 |     |     |
| Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg<br>165 170 175     |     |     |
| Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala<br>180 185 190     |     |     |
| Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly<br>195 200 205     |     |     |
| Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr<br>210 215 220     |     |     |
| Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro<br>225 230 235 240 |     |     |
| Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp<br>245 250 255     |     |     |
| Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu<br>260 265 270     |     |     |
| His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu<br>275 280 285     |     |     |
| Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys<br>290 295 300     |     |     |
| Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser<br>305 310 315 320 |     |     |
| Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu<br>325 330 335     |     |     |
| Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr<br>340 345 350     |     |     |
| Gly Val Tyr Cys Tyr Arg Gln His<br>355 360                                         |     |     |

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

090548-071304

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214  
tgcttcgcta ctgccctc 18

<210> 215  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215  
ttcccttggtg ggttgagg 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
agggctggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagtggag gaaatgag 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg 24

105720-345060

<210> 219

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 219

gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag

45

<210> 220

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 220

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aaa 1503

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<210> 221

<211> 328

<212> PRT

<213> Homo sapiens

<400> 221

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Arg His

FOR "20" 24250650

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly | 20  | 25  | 30  |
| Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala | 35  | 40  | 45  |
| His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val | 50  | 55  | 60  |
| Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu | 65  | 70  | 75  |
| Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp | 85  | 90  | 95  |
| Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg | 100 | 105 | 110 |
| His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp | 115 | 120 | 125 |
| Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly | 130 | 135 | 140 |
| His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr | 145 | 150 | 155 |
| Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp | 165 | 170 | 175 |
| Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu | 180 | 185 | 190 |
| His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr | 195 | 200 | 205 |
| Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu | 210 | 215 | 220 |
| Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala | 225 | 230 | 235 |
| Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn | 245 | 250 | 255 |
| Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro | 260 | 265 | 270 |
| Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu | 275 | 280 | 285 |

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Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcagggcct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

TOE T 20 84 E 50 60



<400> 225  
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
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 aaa 2403

<210> 227

090534B-071301

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

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Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile  
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Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val  
 35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn  
 50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg  
 65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro  
 85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln  
 100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser  
 115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro  
 130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys  
 145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile  
 165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala  
 180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln  
 195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser  
 210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly  
 225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
 245 250 255

0905348.071304

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270  
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
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 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
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 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
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 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
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 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
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Phe Leu Glu Ser Gln Gln  
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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228  
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<210> 229  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229  
ctgctgtcca caggggag 18

<210> 230  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230  
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<210> 231  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231  
gagatagcaa tttccgcc 18

<210> 232

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<211> 18  
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<223> Description of Artificial Sequence: Synthetic  
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<400> 232  
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<210> 233  
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 <212> DNA  
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<223> Description of Artificial Sequence: Synthetic  
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<400> 233  
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24

<210> 234  
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<223> Description of Artificial Sequence: Synthetic  
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<210> 235  
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 <213> Homo sapiens

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 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420  
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<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
 20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
 35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
 50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
 65 70 75 80

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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
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 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
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 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
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 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
                             130                            135                            140  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
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 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
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 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
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 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
                             225                            230                            235                            240  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
                             245                            250                            255  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
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 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
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 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
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 <210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 238  
 ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49  
  
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 gcagagcgga gatgcagcgg cttg 24  
  
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 <400> 241  
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<210> 242  
 <211> 24  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
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24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
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45

<210> 244  
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 <212> DNA  
 <213> Homo Sapien

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 cacacataca ccttcctctc cttcactgaa gactcacagt cactcactct 200  
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<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser  
 35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu  
 50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu  
 65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly  
 80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe  
 95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu  
 110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His  
 125 130 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His  
 140 145 150

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|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Asn | Gln | Leu | Tyr | Arg<br>155 | Ile | Ala | Pro | Arg | Ala<br>160 | Phe | Ser | Gly | Leu | Ser<br>165 |
| Asn | Leu | Leu | Arg | Leu<br>170 | His | Leu | Asn | Ser | Asn<br>175 | Leu | Leu | Arg | Ala | Ile<br>180 |
| Asp | Ser | Arg | Trp | Phe<br>185 | Glu | Met | Leu | Pro | Asn<br>190 | Leu | Glu | Ile | Leu | Met<br>195 |
| Ile | Gly | Gly | Asn | Lys<br>200 | Val | Asp | Ala | Ile | Leu<br>205 | Asp | Met | Asn | Phe | Arg<br>210 |
| Pro | Leu | Ala | Asn | Leu<br>215 | Arg | Ser | Leu | Val | Leu<br>220 | Ala | Gly | Met | Asn | Leu<br>225 |
| Arg | Glu | Ile | Ser | Asp<br>230 | Tyr | Ala | Leu | Glu | Gly<br>235 | Leu | Gln | Ser | Leu | Glu<br>240 |
| Ser | Leu | Ser | Phe | Tyr<br>245 | Asp | Asn | Gln | Leu | Ala<br>250 | Arg | Val | Pro | Arg | Arg<br>255 |
| Ala | Leu | Glu | Gln | Val<br>260 | Pro | Gly | Leu | Lys | Phe<br>265 | Leu | Asp | Leu | Asn | Lys<br>270 |
| Asn | Pro | Leu | Gln | Arg<br>275 | Val | Gly | Pro | Gly | Asp<br>280 | Phe | Ala | Asn | Met | Leu<br>285 |
| His | Leu | Lys | Glu | Leu<br>290 | Gly | Leu | Asn | Asn | Met<br>295 | Glu | Glu | Leu | Val | Ser<br>300 |
| Ile | Asp | Lys | Phe | Ala<br>305 | Leu | Val | Asn | Leu | Pro<br>310 | Glu | Leu | Thr | Lys | Leu<br>315 |
| Asp | Ile | Thr | Asn | Asn<br>320 | Pro | Arg | Leu | Ser | Phe<br>325 | Ile | His | Pro | Arg | Ala<br>330 |
| Phe | His | His | Leu | Pro<br>335 | Gln | Met | Glu | Thr | Leu<br>340 | Met | Leu | Asn | Asn | Asn<br>345 |
| Ala | Leu | Ser | Ala | Leu<br>350 | His | Gln | Gln | Thr | Val<br>355 | Glu | Ser | Leu | Pro | Asn<br>360 |
| Leu | Gln | Glu | Val | Gly<br>365 | Leu | His | Gly | Asn | Pro<br>370 | Ile | Arg | Cys | Asp | Cys<br>375 |
| Val | Ile | Arg | Trp | Ala<br>380 | Asn | Ala | Thr | Gly | Thr<br>385 | Arg | Val | Arg | Phe | Ile<br>390 |
| Glu | Pro | Gln | Ser | Thr<br>395 | Leu | Cys | Ala | Glu | Pro<br>400 | Pro | Asp | Leu | Gln | Arg<br>405 |
| Leu | Pro | Val | Arg | Glu        | Val | Pro | Phe | Arg | Glu        | Met | Thr | Asp | His | Cys        |

|                                     |                         |  |     |     |     |
|-------------------------------------|-------------------------|--|-----|-----|-----|
|                                     | 410                     |  | 415 |     | 420 |
| Leu Pro Leu Ile Ser Pro Arg Ser Phe | Pro Pro Ser Leu Gln Val |  |     |     |     |
| 425                                 | 430                     |  |     | 435 |     |
| Ala Ser Gly Glu Ser Met Val Leu His | Cys Arg Ala Leu Ala Glu |  |     |     |     |
| 440                                 | 445                     |  |     | 450 |     |
| Pro Glu Pro Glu Ile Tyr Trp Val Thr | Pro Ala Gly Leu Arg Leu |  |     |     |     |
| 455                                 | 460                     |  |     | 465 |     |
| Thr Pro Ala His Ala Gly Arg Arg Tyr | Arg Val Tyr Pro Glu Gly |  |     |     |     |
| 470                                 | 475                     |  |     | 480 |     |
| Thr Leu Glu Leu Arg Arg Val Thr Ala | Glu Glu Ala Gly Leu Tyr |  |     |     |     |
| 485                                 | 490                     |  |     | 495 |     |
| Thr Cys Val Ala Gln Asn Leu Val Gly | Ala Asp Thr Lys Thr Val |  |     |     |     |
| 500                                 | 505                     |  |     | 510 |     |
| Ser Val Val Val Gly Arg Ala Leu Leu | Gln Pro Gly Arg Asp Glu |  |     |     |     |
| 515                                 | 520                     |  |     | 525 |     |
| Gly Gln Gly Leu Glu Leu Arg Val Gln | Glu Thr His Pro Tyr His |  |     |     |     |
| 530                                 | 535                     |  |     | 540 |     |
| Ile Leu Leu Ser Trp Val Thr Pro Pro | Asn Thr Val Ser Thr Asn |  |     |     |     |
| 545                                 | 550                     |  |     | 555 |     |
| Leu Thr Trp Ser Ser Ala Ser Ser Leu | Arg Gly Gln Gly Ala Thr |  |     |     |     |
| 560                                 | 565                     |  |     | 570 |     |
| Ala Leu Ala Arg Leu Pro Arg Gly Thr | His Ser Tyr Asn Ile Thr |  |     |     |     |
| 575                                 | 580                     |  |     | 585 |     |
| Arg Leu Leu Gln Ala Thr Glu Tyr Trp | Ala Cys Leu Gln Val Ala |  |     |     |     |
| 590                                 | 595                     |  |     | 600 |     |
| Phe Ala Asp Ala His Thr Gln Leu Ala | Cys Val Trp Ala Arg Thr |  |     |     |     |
| 605                                 | 610                     |  |     | 615 |     |
| Lys Glu Ala Thr Ser Cys His Arg Ala | Leu Gly Asp Arg Pro Gly |  |     |     |     |
| 620                                 | 625                     |  |     | 630 |     |
| Leu Ile Ala Ile Leu Ala Leu Ala Val | Leu Leu Leu Ala Ala Gly |  |     |     |     |
| 635                                 | 640                     |  |     | 645 |     |
| Leu Ala Ala His Leu Gly Thr Gly Gln | Pro Arg Lys Gly Val Gly |  |     |     |     |
| 650                                 | 655                     |  |     | 660 |     |
| Gly Arg Arg Pro Leu Pro Pro Ala Trp | Ala Phe Trp Gly Trp Ser |  |     |     |     |
| 665                                 | 670                     |  |     | 675 |     |

FOET 20-84E50660

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                     680                    685                    690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
                     695                    700                    705

Leu Pro Pro Leu Ser Gln Asn Ser  
                     710

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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

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<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

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<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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090548-01301  
 10E120-8HE50650

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 gcctcctgca gaacctccag aacctagcca tcacggccaa ccgcatcgag 1450



|            |            |            |             |            |      |
|------------|------------|------------|-------------|------------|------|
| acgctccctc | cggagctctt | ccagtgccgg | aagctgcggg  | ccctgcacct | 1500 |
| gggcaacaac | gtgctgcagt | cactgccctc | cagggtgggc  | gagctgacca | 1550 |
| acctgacgca | gatcgagctg | cggggcaacc | ggctggagtg  | cctgcctgtg | 1600 |
| gagctgggcg | agtgccct   | gctcaagcgc | agcggcttgg  | tggtggagga | 1650 |
| ggacctgttc | aacacactgc | cacccgaggt | gaaggagcgg  | ctgtggaggg | 1700 |
| ctgacaagga | gcaggcctga | gcgaggccgg | cccagcacag  | caagcagcag | 1750 |
| gaccgctgcc | cagtcctcag | gcccggaggg | gcaggcctag  | cttctcccag | 1800 |
| aactcccgga | cagccaggac | agcctcgcgg | ctgggcagga  | gcctggggcc | 1850 |
| gcttgtgagt | caggccagag | cgagaggaca | gtatctgtgg  | ggctggcccc | 1900 |
| ttttctccct | ctgagactca | cgtccccag  | ggcaagtgct  | tgtggaggag | 1950 |
| agcaagtctc | aagagcgcag | tatttgata  | atcagggctc  | cctccctgga | 2000 |
| ggccagctct | gccccagggg | ctgagctgcc | accagaggtc  | ctgggacctt | 2050 |
| cactttagtt | cttggtat   | atttttctcc | atctcccacc  | tccttcatcc | 2100 |
| agataactta | tacattccca | agaaagtcca | gccagatgg   | aaggtgtcca | 2150 |
| gggaaaggtg | ggctgccttt | tccccttgtc | cttatttagc  | gatgccgccg | 2200 |
| ggcatttaac | accacactgg | acttcagcag | agtgggccgg  | ggcgaaccag | 2250 |
| ccatgggacg | gtcaccacgc | agtgccgggc | tgggctctgc  | ggtgcggtcc | 2300 |
| acgggagagc | aggcctccag | ctggaaaggc | caggcctgga  | gcttgccctt | 2350 |
| tcagtTTTTG | tggcagTTTT | agTTTTTtGt | TTTTTTTTTT  | TTTaatcaaa | 2400 |
| aaacaatttt | TTTTAAAAA  | aagctttgaa | aatggatgg   | ttgggtatta | 2450 |
| aaaagaaaaa | aaaaacttaa | aaaaaaaaag | acactaacgg  | ccagtgagtt | 2500 |
| ggagtctcag | ggcaggggtg | cagtttccct | tgagcaaagc  | agccagacgt | 2550 |
| tgaactgtgt | ttcctttccc | tgggcgcagg | gtgcaggggtg | tcttccggat | 2600 |
| ctggtgtgac | cttggtccag | gagttctatt | tgttcctggg  | gagggaggtt | 2650 |
| TTTTTgtttg | TTTTTTgggt | TTTTTTggtg | tcttgTTTTc  | TTTctcctcc | 2700 |
| atgtgtcttg | gcaggcactc | atttctgtgg | ctgtcggcca  | gagggaatgt | 2750 |
| tctggagctg | ccaaggaggg | aggagactcg | ggttggctaa  | tccccgatg  | 2800 |

aacggtgctc cattcgaccc tcccctcctc gtgcoctgcc tgccctctcca 2850  
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 a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Arg | Gln | Thr | Ile | Ile | Lys | Val | Ile | Lys | Phe | Ile | Leu | Ile | Ile | 1  | 5  | 10 | 15 |
| Cys | Tyr | Thr | Val | Tyr | Tyr | Val | His | Asn | Ile | Lys | Phe | Asp | Val | Asp | 20 | 25 | 30 |    |
| Cys | Thr | Val | Asp | Ile | Glu | Ser | Leu | Thr | Gly | Tyr | Arg | Thr | Tyr | Arg | 35 | 40 | 45 |    |
| Cys | Ala | His | Pro | Leu | Ala | Thr | Leu | Phe | Lys | Ile | Leu | Ala | Ser | Phe | 50 | 55 | 60 |    |
| Tyr | Ile | Ser | Leu | Val | Ile | Phe | Tyr | Gly | Leu | Ile | Cys | Met | Tyr | Thr | 65 | 70 | 75 |    |
| Leu | Trp | Trp | Met | Leu | Arg | Arg | Ser | Leu | Lys | Lys | Tyr | Ser | Phe | Glu | 80 | 85 | 90 |    |
| Ser | Ile | Arg | Glu | Glu | Ser | Ser | Tyr | Ser | Asp | Ile | Pro | Asp | Val | Lys |    |    |    |    |

090548-07301

|                                                             |     |  |     |  |     |
|-------------------------------------------------------------|-----|--|-----|--|-----|
|                                                             | 95  |  | 100 |  | 105 |
| Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro | 110 |  | 115 |  | 120 |
| Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu | 125 |  | 130 |  | 135 |
| Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp | 140 |  | 145 |  | 150 |
| Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu | 155 |  | 160 |  | 165 |
| Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp | 170 |  | 175 |  | 180 |
| Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val | 185 |  | 190 |  | 195 |
| Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu | 200 |  | 205 |  | 210 |
| Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala | 215 |  | 220 |  | 225 |
| Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp | 230 |  | 235 |  | 240 |
| Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu | 245 |  | 250 |  | 255 |
| Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr | 260 |  | 265 |  | 270 |
| Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu | 275 |  | 280 |  | 285 |
| Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp | 290 |  | 295 |  | 300 |
| Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr | 305 |  | 310 |  | 315 |
| Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr | 320 |  | 325 |  | 330 |
| Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser | 335 |  | 340 |  | 345 |
| Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn | 350 |  | 355 |  | 360 |

TDE120"84E50660

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His  
 365 370 375  
 Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile  
 380 385 390  
 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
 395 400 405  
 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
 410 415 420  
 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
 425 430 435  
 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
 440 445 450  
 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
 455 460 465  
 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
 470 475 480  
 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
 485 490 495  
 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly  
 500 505 510  
 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp  
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<210> 251

<211> 20

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 252

<211> 24

090548.031301

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

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<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

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<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Ala | Leu | Arg | Arg | Ser | Pro | Val | Pro | Arg | Trp | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Leu | Pro | Leu | Leu | Leu | Gly | Leu | Asn | Ala | Gly | Ala | Val | Ile | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Trp | Pro | Thr | Glu | Glu | Gly | Lys | Glu | Val | Trp | Asp | Tyr | Val | Thr | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Lys | Asp | Ala | Tyr | Met | Phe | Trp | Trp | Leu | Tyr | Tyr | Ala | Thr | Asn |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |  |
| Ser | Cys | Lys | Asn | Phe | Ser | Glu | Leu | Pro | Leu | Val | Met | Trp | Leu | Gln |  |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |  |
| Gly | Gly | Pro | Gly | Gly | Ser | Ser | Thr | Gly | Phe | Gly | Asn | Phe | Glu | Glu |  |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |  |
| Ile | Gly | Pro | Leu | Asp | Ser | Asp | Leu | Lys | Pro | Arg | Lys | Thr | Thr | Trp |  |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |  |
| Leu | Gln | Ala | Ala | Ser | Leu | Leu | Phe | Val | Asp | Asn | Pro | Val | Gly | Thr |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |  |
| Gly | Phe | Ser | Tyr | Val | Asn | Gly | Ser | Gly | Ala | Tyr | Ala | Lys | Asp | Leu |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |  |
| Ala | Met | Val | Ala | Ser | Asp | Met | Met | Val | Leu | Leu | Lys | Thr | Phe | Phe |  |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |  |
| Ser | Cys | His | Lys | Glu | Phe | Gln | Thr | Val | Pro | Phe | Tyr | Ile | Phe | Ser |  |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |  |
| Glu | Ser | Tyr | Gly | Gly | Lys | Met | Ala | Ala | Gly | Ile | Gly | Leu | Glu | Leu |  |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |  |
| Tyr | Lys | Ala | Ile | Gln | Arg | Gly | Thr | Ile | Lys | Cys | Asn | Phe | Ala | Gly |  |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |  |
| Val | Ala | Leu | Gly | Asp | Ser | Trp | Ile | Ser | Pro | Val | Asp | Ser | Val | Leu |  |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |  |
| Ser | Trp | Gly | Pro | Tyr | Leu | Tyr | Ser | Met | Ser | Leu | Leu | Glu | Asp | Lys |  |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |  |
| Gly | Leu | Ala | Glu | Val | Ser | Lys | Val | Ala | Glu | Gln | Val | Leu | Asn | Ala |  |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Val | Asn | Lys | Gly | Leu | Tyr | Arg | Glu | Ala | Thr | Glu | Leu | Trp | Gly | Lys |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |  |
| Ala | Glu | Met | Ile | Ile | Glu | Gln | Asn | Thr | Asp | Gly | Val | Asn | Phe | Tyr |  |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |  |
| Asn | Ile | Leu | Thr | Lys | Ser | Thr | Pro | Thr | Ser | Thr | Met | Glu | Ser | Ser |  |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |  |
| Leu | Glu | Phe | Thr | Gln | Ser | His | Leu | Val | Cys | Leu | Cys | Gln | Arg | His |  |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |  |
| Val | Arg | His | Leu | Gln | Arg | Asp | Ala | Leu | Ser | Gln | Leu | Met | Asn | Gly |  |

TOEFL-074301-84E50660

|                                     |                         |     |
|-------------------------------------|-------------------------|-----|
| 305                                 | 310                     | 315 |
| Pro Ile Arg Lys Lys Leu Lys Ile Ile | Pro Glu Asp Gln Ser Trp |     |
| 320                                 | 325                     | 330 |
| Gly Gly Gln Ala Thr Asn Val Phe Val | Asn Met Glu Glu Asp Phe |     |
| 335                                 | 340                     | 345 |
| Met Lys Pro Val Ile Ser Ile Val Asp | Glu Leu Leu Glu Ala Gly |     |
| 350                                 | 355                     | 360 |
| Ile Asn Val Thr Val Tyr Asn Gly Gln | Leu Asp Leu Ile Val Asp |     |
| 365                                 | 370                     | 375 |
| Thr Met Gly Gln Glu Ala Trp Val Arg | Lys Leu Lys Trp Pro Glu |     |
| 380                                 | 385                     | 390 |
| Leu Pro Lys Phe Ser Gln Leu Lys Trp | Lys Ala Leu Tyr Ser Asp |     |
| 395                                 | 400                     | 405 |
| Pro Lys Ser Leu Glu Thr Ser Ala Phe | Val Lys Ser Tyr Lys Asn |     |
| 410                                 | 415                     | 420 |
| Leu Ala Phe Tyr Trp Ile Leu Lys Ala | Gly His Met Val Pro Ser |     |
| 425                                 | 430                     | 435 |
| Asp Gln Gly Asp Met Ala Leu Lys Met | Met Arg Leu Val Thr Gln |     |
| 440                                 | 445                     | 450 |

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgcgcc tgctcagcca ccgctgggca 250

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gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

09905348-031301



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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

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 35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg  
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Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg  
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Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu  
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0905348-071301

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
 95 100 105  
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 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
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 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
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 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
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&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

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09905348-01301

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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Gln | Ala | Cys | Leu | Leu | Gly | Leu | Phe | Ala | Leu | Ile | Leu |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

09905349.074304

|                                                             |     |  |     |  |     |
|-------------------------------------------------------------|-----|--|-----|--|-----|
|                                                             | 20  |  | 25  |  | 30  |
| Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu | 35  |  | 40  |  | 45  |
| Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg | 50  |  | 55  |  | 60  |
| Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln | 65  |  | 70  |  | 75  |
| Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg | 80  |  | 85  |  | 90  |
| Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala | 95  |  | 100 |  | 105 |
| Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu | 110 |  | 115 |  | 120 |
| Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly | 125 |  | 130 |  | 135 |
| Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val | 140 |  | 145 |  | 150 |
| Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro | 155 |  | 160 |  | 165 |
| His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser | 170 |  | 175 |  | 180 |
| Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly | 185 |  | 190 |  | 195 |
| Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn | 200 |  | 205 |  | 210 |
| Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln | 215 |  | 220 |  | 225 |
| Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu | 230 |  | 235 |  | 240 |
| Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala | 245 |  | 250 |  | 255 |
| Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly | 260 |  | 265 |  | 270 |
| Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala | 275 |  | 280 |  | 285 |

FOR "345050"

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ile | Ser | Thr | Trp | Val | Tyr | Ser | Ser | Pro | Gly | Arg | His | Glu | Gly |  |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |  |
| Gln | Glu | Pro | Phe | Leu | Gln | Trp | Leu | Met | Leu | Leu | Ser | Asn | Glu | Ser |  |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |  |
| Ala | Leu | Pro | His | Val | His | Thr | Val | Ser | Tyr | Gly | Asp | Asp | Glu | Asp |  |
|     |     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |  |
| Ser | Leu | Ser | Ser | Ala | Tyr | Ile | Gln | Arg | Val | Asn | Thr | Glu | Leu | Met |  |
|     |     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |  |
| Lys | Ala | Ala | Ala | Arg | Gly | Leu | Thr | Leu | Leu | Phe | Ala | Ser | Gly | Asp |  |
|     |     |     |     | 350 |     |     |     |     | 355 |     |     |     |     | 360 |  |
| Ser | Gly | Ala | Gly | Cys | Trp | Ser | Val | Ser | Gly | Arg | His | Gln | Phe | Arg |  |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |  |
| Pro | Thr | Phe | Pro | Ala | Ser | Ser | Pro | Tyr | Val | Thr | Thr | Val | Gly | Gly |  |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |  |
| Thr | Ser | Phe | Gln | Glu | Pro | Phe | Leu | Ile | Thr | Asn | Glu | Ile | Val | Asp |  |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |  |
| Tyr | Ile | Ser | Gly | Gly | Gly | Phe | Ser | Asn | Val | Phe | Pro | Arg | Pro | Ser |  |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |  |
| Tyr | Gln | Glu | Glu | Ala | Val | Thr | Lys | Phe | Leu | Ser | Ser | Ser | Pro | His |  |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |  |
| Leu | Pro | Pro | Ser | Ser | Tyr | Phe | Asn | Ala | Ser | Gly | Arg | Ala | Tyr | Pro |  |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |  |
| Asp | Val | Ala | Ala | Leu | Ser | Asp | Gly | Tyr | Trp | Val | Val | Ser | Asn | Arg |  |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |  |
| Val | Pro | Ile | Pro | Trp | Val | Ser | Gly | Thr | Ser | Ala | Ser | Thr | Pro | Val |  |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
| Phe | Gly | Gly | Ile | Leu | Ser | Leu | Ile | Asn | Glu | His | Arg | Ile | Leu | Ser |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |  |
| Gly | Arg | Pro | Pro | Leu | Gly | Phe | Leu | Asn | Pro | Arg | Leu | Tyr | Gln | Gln |  |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |  |
| His | Gly | Ala | Gly | Leu | Phe | Asp | Val | Thr | Arg | Gly | Cys | His | Glu | Ser |  |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |  |
| Cys | Leu | Asp | Glu | Glu | Val | Glu | Gly | Gln | Gly | Phe | Cys | Ser | Gly | Pro |  |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |  |
| Gly | Trp | Asp | Pro | Val | Thr | Gly | Trp | Gly | Thr | Pro | Thr | Ser | Gln | Leu |  |
|     |     |     |     | 545 |     |     |     |     | 550 |     |     |     |     | 555 |  |

09905348-071304

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

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F0905348.071301

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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Ile | Pro | Gly | Leu | Leu | Phe | Leu | Leu | Phe | Phe | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ala | Val | Gly | Gln | Val | Ser | Pro | Tyr | Ser | Ala | Pro | Trp | Lys | Pro |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Trp | Pro | Ala | Tyr | Arg | Leu | Pro | Val | Val | Leu | Pro | Gln | Ser | Thr |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Leu | Ala | Lys | Pro | Asp | Phe | Gly | Ala | Glu | Ala | Lys | Leu | Glu |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Ser | Ser | Cys | Gly | Pro | Gln | Cys | His | Lys | Gly | Thr | Pro | Leu |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Tyr | Glu | Glu | Ala | Lys | Gln | Tyr | Leu | Ser | Tyr | Glu | Thr | Leu |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Asn | Gly | Ser | Arg | Thr | Glu | Thr | Gln | Val | Gly | Ile | Tyr | Ile |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ser | Ser | Gly | Asp | Gly | Ala | Gln | His | Arg | Asp | Ser | Gly | Ser |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |

090548.01301



|                 |                                             |     |     |     |
|-----------------|---------------------------------------------|-----|-----|-----|
| Ser Gly Lys Ser | Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser | 125 | 130 | 135 |
| Arg Phe Ser Ile | Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe | 140 | 145 | 150 |
| Ser Thr Ser Val | Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val | 155 | 160 | 165 |
| Ala Glu Lys His | Val Leu Thr Ala Ala His Cys Ile His Asp Gly | 170 | 175 | 180 |
| Lys Thr Tyr Val | Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu | 185 | 190 | 195 |
| Lys Pro Lys Phe | Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr | 200 | 205 | 210 |
| Ser Ala Met Pro | Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys | 215 | 220 | 225 |
| Arg Thr His Val | Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp | 230 | 235 | 240 |
| Ile Gly Met Asp | Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro | 245 | 250 | 255 |
| His Lys Arg Lys | Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys | 260 | 265 | 270 |
| Gln Leu Pro Gly | Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp | 275 | 280 | 285 |
| Arg Pro Gly Asn | Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu | 290 | 295 | 300 |
| Thr Tyr Asp Leu | Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala | 305 | 310 | 315 |
| Ser Gly Ser Gly | Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln | 320 | 325 | 330 |
| Lys Trp Glu Arg | Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp | 335 | 340 | 345 |
| Val Asp Met Asn | Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg | 350 | 355 | 360 |
| Ile Thr Pro Leu | Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly | 365 | 370 | 375 |
| Asn Tyr Leu Asp | Cys Arg Glu Gly                             | 380 |     |     |

0905348.071301  
FOETCO-BHE50660

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 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
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 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
 ttgtggggcg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
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 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
 cgggtccaga aggtgggtgt tgctgggtg gagccccacc ctgtgtattc 450  
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctgagcgct 500  
 ccatacagtt ctgagagcgg gtccctgcca tctgcctacc tgatgcctct 550  
 atccacctcc ctccaaacac ccaactgctg atctcaggct gggggagcat 600  
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
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<213> Homo Sapien.

<400> 263

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| Met | Val | Val | Ser | Gly | Ala | Pro | Pro | Ala | Leu | Gly | Gly | Gly | Cys | Leu | 1   | 5   | 10  | 15 |
| Gly | Thr | Phe | Thr | Ser | Leu | Leu | Leu | Leu | Ala | Ser | Thr | Ala | Ile | Leu | 20  | 25  | 30  |    |
| Asn | Ala | Ala | Arg | Ile | Pro | Val | Pro | Pro | Ala | Cys | Gly | Lys | Pro | Gln | 35  | 40  | 45  |    |
| Gln | Leu | Asn | Arg | Val | Val | Gly | Gly | Glu | Asp | Ser | Thr | Asp | Ser | Glu | 50  | 55  | 60  |    |
| Trp | Pro | Trp | Ile | Val | Ser | Ile | Gln | Lys | Asn | Gly | Thr | His | His | Cys | 65  | 70  | 75  |    |
| Ala | Gly | Ser | Leu | Leu | Thr | Ser | Arg | Trp | Val | Ile | Thr | Ala | Ala | His | 80  | 85  | 90  |    |
| Cys | Phe | Lys | Asp | Asn | Leu | Asn | Lys | Pro | Tyr | Leu | Phe | Ser | Val | Leu | 95  | 100 | 105 |    |
| Leu | Gly | Ala | Trp | Gln | Leu | Gly | Asn | Pro | Gly | Ser | Arg | Ser | Gln | Lys | 110 | 115 | 120 |    |
| Val | Gly | Val | Ala | Trp | Val | Glu | Pro | His | Pro | Val | Tyr | Ser | Trp | Lys | 125 | 130 | 135 |    |
| Glu | Gly | Ala | Cys | Ala | Asp | Ile | Ala | Leu | Val | Arg | Leu | Glu | Arg | Ser | 140 | 145 | 150 |    |
| Ile | Gln | Phe | Ser | Glu | Arg | Val | Leu | Pro | Ile | Cys | Leu | Pro | Asp | Ala | 155 | 160 | 165 |    |
| Ser | Ile | His | Leu | Pro | Pro | Asn | Thr | His | Cys | Trp | Ile | Ser | Gly | Trp | 170 | 175 | 180 |    |

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|                                                             |     |     |     |
|-------------------------------------------------------------|-----|-----|-----|
| Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu | 185 | 190 | 195 |
| Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His | 200 | 205 | 210 |
| Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met | 215 | 220 | 225 |
| Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly | 230 | 235 | 240 |
| Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu | 245 | 250 | 255 |
| Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn | 260 | 265 | 270 |
| Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val | 275 | 280 | 285 |
| Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly | 290 | 295 | 300 |
| Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala | 305 | 310 | 315 |

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<211> 24

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<220>

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<400> 264

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<210> 266

<211> 24

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<210> 273  
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<212> DNA

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<212> PRT

<213> Homo Sapien

<400> 285

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| Met | His | Gly | Ser | Cys | Ser | Phe | Leu | Met | Leu | Leu | Leu | Pro | Leu | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Leu | Leu | Leu | Val | Ala | Thr | Thr | Gly | Pro | Val | Gly | Ala | Leu | Thr | Asp |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |  |
| Glu | Glu | Lys | Arg | Leu | Met | Val | Glu | Leu | His | Asn | Leu | Tyr | Arg | Ala |  |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |  |
| Gln | Val | Ser | Pro | Thr | Ala | Ser | Asp | Met | Leu | His | Met | Arg | Trp | Asp |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |  |
| Glu | Glu | Leu | Ala | Ala | Phe | Ala | Lys | Ala | Tyr | Ala | Arg | Gln | Cys | Val |  |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |  |
| Trp | Gly | His | Asn | Lys | Glu | Arg | Gly | Arg | Arg | Gly | Glu | Asn | Leu | Phe |  |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |  |
| Ala | Ile | Thr | Asp | Glu | Gly | Met | Asp | Val | Pro | Leu | Ala | Met | Glu | Glu |  |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |  |
| Trp | His | His | Glu | Arg | Glu | His | Tyr | Asn | Leu | Ser | Ala | Ala | Thr | Cys |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |  |
| Ser | Pro | Gly | Gln | Met | Cys | Gly | His | Tyr | Thr | Gln | Val | Val | Trp | Ala |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |  |

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|                 |                     |                         |
|-----------------|---------------------|-------------------------|
| Lys Thr Glu Arg | Ile Gly Cys Gly Ser | His Phe Cys Glu Lys Leu |
|                 | 140                 | 145 150                 |
| Gln Gly Val Glu | Glu Thr Asn Ile Glu | Leu Leu Val Cys Asn Tyr |
|                 | 155                 | 160 165                 |
| Glu Pro Pro Gly | Asn Val Lys Gly Lys | Arg Pro Tyr Gln Glu Gly |
|                 | 170                 | 175 180                 |
| Thr Pro Cys Ser | Gln Cys Pro Ser Gly | Tyr His Cys Lys Asn Ser |
|                 | 185                 | 190 195                 |
| Leu Cys Glu Pro | Ile Gly Ser Pro Glu | Asp Ala Gln Asp Leu Pro |
|                 | 200                 | 205 210                 |
| Tyr Leu Val Thr | Glu Ala Pro Ser Phe | Arg Ala Thr Glu Ala Ser |
|                 | 215                 | 220 225                 |
| Asp Ser Arg Lys | Met Gly Thr Pro Ser | Ser Leu Ala Thr Gly Ile |
|                 | 230                 | 235 240                 |
| Pro Ala Phe Leu | Val Thr Glu Val Ser | Gly Ser Leu Ala Thr Lys |
|                 | 245                 | 250 255                 |
| Ala Leu Pro Ala | Val Glu Thr Gln Ala | Pro Thr Ser Leu Ala Thr |
|                 | 260                 | 265 270                 |
| Lys Asp Pro Pro | Ser Met Ala Thr Glu | Ala Pro Pro Cys Val Thr |
|                 | 275                 | 280 285                 |
| Thr Glu Val Pro | Ser Ile Leu Ala Ala | His Ser Leu Pro Ser Leu |
|                 | 290                 | 295 300                 |
| Asp Glu Glu Pro | Val Thr Phe Pro Lys | Ser Thr His Val Pro Ile |
|                 | 305                 | 310 315                 |
| Pro Lys Ser Ala | Asp Lys Val Thr Asp | Lys Thr Lys Val Pro Ser |
|                 | 320                 | 325 330                 |
| Arg Ser Pro Glu | Asn Ser Leu Asp Pro | Lys Met Ser Leu Thr Gly |
|                 | 335                 | 340 345                 |
| Ala Arg Glu Leu | Leu Pro His Ala Gln | Glu Glu Ala Glu Ala Glu |
|                 | 350                 | 355 360                 |
| Ala Glu Leu Pro | Pro Ser Ser Glu Val | Leu Ala Ser Val Phe Pro |
|                 | 365                 | 370 375                 |
| Ala Gln Asp Lys | Pro Gly Glu Leu Gln | Ala Thr Leu Asp His Thr |
|                 | 380                 | 385 390                 |
| Gly His Thr Ser | Ser Lys Ser Leu Pro | Asn Phe Pro Asn Thr Ser |
|                 | 395                 | 400 405                 |

TOE720" BHE50660



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| Met | Val | Asp | Val | Leu | Leu | Leu | Phe | Ser | Leu | Cys | Leu | Leu | Phe | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Arg | Pro | Asp | Leu | Ser | His | Asn | Arg | Leu | Ser | Phe | Ile | Lys |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Ser | Met | Ser | His | Leu | Gln | Ser | Leu | Arg | Glu | Val | Lys | Leu | 35  | 40  | 45  |
| Asn | Asn | Asn | Glu | Leu | Glu | Thr | Ile | Pro | Asn | Leu | Gly | Pro | Val | Ser | 50  | 55  | 60  |
| Ala | Asn | Ile | Thr | Leu | Leu | Ser | Leu | Ala | Gly | Asn | Arg | Ile | Val | Glu | 65  | 70  | 75  |
| Ile | Leu | Pro | Glu | His | Leu | Lys | Glu | Phe | Gln | Ser | Leu | Glu | Thr | Leu | 80  | 85  | 90  |
| Asp | Leu | Ser | Ser | Asn | Asn | Ile | Ser | Glu | Leu | Gln | Thr | Ala | Phe | Pro | 95  | 100 | 105 |
| Ala | Leu | Gln | Leu | Lys | Tyr | Leu | Tyr | Leu | Asn | Ser | Asn | Arg | Val | Thr | 110 | 115 | 120 |
| Ser | Met | Glu | Pro | Gly | Tyr | Phe | Asp | Asn | Leu | Ala | Asn | Thr | Leu | Leu | 125 | 130 | 135 |
| Val | Leu | Lys | Leu | Asn | Arg | Asn | Arg | Ile | Ser | Ala | Ile | Pro | Pro | Lys | 140 | 145 | 150 |
| Met | Phe | Lys | Leu | Pro | Gln | Leu | Gln | His | Leu | Glu | Leu | Asn | Arg | Asn | 155 | 160 | 165 |
| Lys | Ile | Lys | Asn | Val | Asp | Gly | Leu | Thr | Phe | Gln | Gly | Leu | Gly | Ala | 170 | 175 | 180 |
| Leu | Lys | Ser | Leu | Lys | Met | Gln | Arg | Asn | Gly | Val | Thr | Lys | Leu | Met | 185 | 190 | 195 |
| Asp | Gly | Ala | Phe | Trp | Gly | Leu | Ser | Asn | Met | Glu | Ile | Leu | Gln | Leu | 200 | 205 | 210 |
| Asp | His | Asn | Asn | Leu | Thr | Glu | Ile | Thr | Lys | Gly | Trp | Leu | Tyr | Gly | 215 | 220 | 225 |
| Leu | Leu | Met | Leu | Gln | Glu | Leu | His | Leu | Ser | Gln | Asn | Ala | Ile | Asn | 230 | 235 | 240 |
| Arg | Ile | Ser | Pro | Asp | Ala | Trp | Glu | Phe | Cys | Gln | Lys | Leu | Ser | Glu | 245 | 250 | 255 |
| Leu | Asp | Leu | Thr | Phe | Asn | His | Leu | Ser | Arg | Leu | Asp | Asp | Ser | Ser | 260 | 265 | 270 |
| Phe | Leu | Gly | Leu | Ser | Leu | Leu | Asn | Thr | Leu | His | Ile | Gly | Asn | Asn | 275 | 280 | 285 |
| Arg | Val | Ser | Tyr | Ile | Ala | Asp | Cys | Ala | Phe | Arg | Gly | Leu | Ser | Ser |     |     |     |

0905348.071361  
FOET 20" 84E50660



|     |     |     |     |            |     |     |     |     |            |     |     |     |     |            |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
|     |     |     |     | 290        |     |     |     |     | 295        |     |     |     |     | 300        |
| Leu | Lys | Thr | Leu | Asp<br>305 | Leu | Lys | Asn | Asn | Glu<br>310 | Ile | Ser | Trp | Thr | Ile<br>315 |
| Glu | Asp | Met | Asn | Gly<br>320 | Ala | Phe | Ser | Gly | Leu<br>325 | Asp | Lys | Leu | Arg | Arg<br>330 |
| Leu | Ile | Leu | Gln | Gly<br>335 | Asn | Arg | Ile | Arg | Ser<br>340 | Ile | Thr | Lys | Lys | Ala<br>345 |
| Phe | Thr | Gly | Leu | Asp<br>350 | Ala | Leu | Glu | His | Leu<br>355 | Asp | Leu | Ser | Asp | Asn<br>360 |
| Ala | Ile | Met | Ser | Leu<br>365 | Gln | Gly | Asn | Ala | Phe<br>370 | Ser | Gln | Met | Lys | Lys<br>375 |
| Leu | Gln | Gln | Leu | His<br>380 | Leu | Asn | Thr | Ser | Ser<br>385 | Leu | Leu | Cys | Asp | Cys<br>390 |
| Gln | Leu | Lys | Trp | Leu<br>395 | Pro | Gln | Trp | Val | Ala<br>400 | Glu | Asn | Asn | Phe | Gln<br>405 |
| Ser | Phe | Val | Asn | Ala<br>410 | Ser | Cys | Ala | His | Pro<br>415 | Gln | Leu | Leu | Lys | Gly<br>420 |
| Arg | Ser | Ile | Phe | Ala<br>425 | Val | Ser | Pro | Asp | Gly<br>430 | Phe | Val | Cys | Asp | Asp<br>435 |
| Phe | Pro | Lys | Pro | Gln<br>440 | Ile | Thr | Val | Gln | Pro<br>445 | Glu | Thr | Gln | Ser | Ala<br>450 |
| Ile | Lys | Gly | Ser | Asn<br>455 | Leu | Ser | Phe | Ile | Cys<br>460 | Ser | Ala | Ala | Ser | Ser<br>465 |
| Ser | Asp | Ser | Pro | Met<br>470 | Thr | Phe | Ala | Trp | Lys<br>475 | Lys | Asp | Asn | Glu | Leu<br>480 |
| Leu | His | Asp | Ala | Glu<br>485 | Met | Glu | Asn | Tyr | Ala<br>490 | His | Leu | Arg | Ala | Gln<br>495 |
| Gly | Gly | Glu | Val | Met<br>500 | Glu | Tyr | Thr | Thr | Ile<br>505 | Leu | Arg | Leu | Arg | Glu<br>510 |
| Val | Glu | Phe | Ala | Ser<br>515 | Glu | Gly | Lys | Tyr | Gln<br>520 | Cys | Val | Ile | Ser | Asn<br>525 |
| His | Phe | Gly | Ser | Ser<br>530 | Tyr | Ser | Val | Lys | Ala<br>535 | Lys | Leu | Thr | Val | Asn<br>540 |
| Met | Leu | Pro | Ser | Phe<br>545 | Thr | Lys | Thr | Pro | Met<br>550 | Asp | Leu | Thr | Ile | Arg<br>555 |

|                 |                     |                     |     |
|-----------------|---------------------|---------------------|-----|
| Ala Gly Ala Met | Ala Arg Leu Glu Cys | Ala Ala Val Gly His | Pro |
| 560             | 565                 |                     | 570 |
| Ala Pro Gln Ile | Ala Trp Gln Lys Asp | Gly Gly Thr Asp Phe | Pro |
| 575             | 580                 |                     | 585 |
| Ala Ala Arg Glu | Arg Arg Met His Val | Met Pro Glu Asp Asp | Val |
| 590             | 595                 |                     | 600 |
| Phe Phe Ile Val | Asp Val Lys Ile Glu | Asp Ile Gly Val Tyr | Ser |
| 605             | 610                 |                     | 615 |
| Cys Thr Ala Gln | Asn Ser Ala Gly Ser | Ile Ser Ala Asn Ala | Thr |
| 620             | 625                 |                     | 630 |
| Leu Thr Val Leu | Glu Thr Pro Ser Phe | Leu Arg Pro Leu Leu | Asp |
| 635             | 640                 |                     | 645 |
| Arg Thr Val Thr | Lys Gly Glu Thr Ala | Val Leu Gln Cys Ile | Ala |
| 650             | 655                 |                     | 660 |
| Gly Gly Ser Pro | Pro Pro Lys Leu Asn | Trp Thr Lys Asp Asp | Ser |
| 665             | 670                 |                     | 675 |
| Pro Leu Val Val | Thr Glu Arg His Phe | Phe Ala Ala Gly Asn | Gln |
| 680             | 685                 |                     | 690 |
| Leu Leu Ile Ile | Val Asp Ser Asp Val | Ser Asp Ala Gly Lys | Tyr |
| 695             | 700                 |                     | 705 |
| Thr Cys Glu Met | Ser Asn Thr Leu Gly | Thr Glu Arg Gly Asn | Val |
| 710             | 715                 |                     | 720 |
| Arg Leu Ser Val | Ile Pro Thr Pro Thr | Cys Asp Ser Pro Gln | Met |
| 725             | 730                 |                     | 735 |
| Thr Ala Pro Ser | Leu Asp Asp Asp Gly | Trp Ala Thr Val Gly | Val |
| 740             | 745                 |                     | 750 |
| Val Ile Ile Ala | Val Val Cys Cys Val | Val Gly Thr Ser Leu | Val |
| 755             | 760                 |                     | 765 |
| Trp Val Val Ile | Ile Tyr His Thr Arg | Arg Arg Asn Glu Asp | Cys |
| 770             | 775                 |                     | 780 |
| Ser Ile Thr Asn | Thr Asp Glu Thr Asn | Leu Pro Ala Asp Ile | Pro |
| 785             | 790                 |                     | 795 |
| Ser Tyr Leu Ser | Ser Gln Gly Thr Leu | Ala Asp Arg Gln Asp | Gly |
| 800             | 805                 |                     | 810 |

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 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
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 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
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 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
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 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
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 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
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&lt;211&gt; 2906

TOE7'0" 84E50660

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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<212> PRT

<213> Homo Sapien

<400> 292

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Leu | Asn | Lys | Met | Thr | Leu | His | Pro | Gln | Gln | Ile | Met | Ile | Gly | 1   | 5   | 10  | 15 |
| Pro | Arg | Phe | Asn | Arg | Ala | Leu | Phe | Asp | Pro | Leu | Leu | Val | Val | Leu | 20  | 25  | 30  |    |
| Leu | Ala | Leu | Gln | Leu | Leu | Val | Val | Ala | Gly | Leu | Val | Arg | Ala | Gln | 35  | 40  | 45  |    |
| Thr | Cys | Pro | Ser | Val | Cys | Ser | Cys | Ser | Asn | Gln | Phe | Ser | Lys | Val | 50  | 55  | 60  |    |
| Ile | Cys | Val | Arg | Lys | Asn | Leu | Arg | Glu | Val | Pro | Asp | Gly | Ile | Ser | 65  | 70  | 75  |    |
| Thr | Asn | Thr | Arg | Leu | Leu | Asn | Leu | His | Glu | Asn | Gln | Ile | Gln | Ile | 80  | 85  | 90  |    |
| Ile | Lys | Val | Asn | Ser | Phe | Lys | His | Leu | Arg | His | Leu | Glu | Ile | Leu | 95  | 100 | 105 |    |
| Gln | Leu | Ser | Arg | Asn | His | Ile | Arg | Thr | Ile | Glu | Ile | Gly | Ala | Phe | 110 | 115 | 120 |    |
| Asn | Gly | Leu | Ala | Asn | Leu | Asn | Thr | Leu | Glu | Leu | Phe | Asp | Asn | Arg | 125 | 130 | 135 |    |
| Leu | Thr | Thr | Ile | Pro | Asn | Gly | Ala | Phe | Val | Tyr | Leu | Ser | Lys | Leu | 140 | 145 | 150 |    |
| Lys | Glu | Leu | Trp | Leu | Arg | Asn | Asn | Pro | Ile | Glu | Ser | Ile | Pro | Ser |     |     |     |    |

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|                                     |                         |     |
|-------------------------------------|-------------------------|-----|
| 155                                 | 160                     | 165 |
| Tyr Ala Phe Asn Arg Ile Pro Ser Leu | Arg Arg Leu Asp Leu Gly |     |
| 170                                 | 175                     | 180 |
| Glu Leu Lys Arg Leu Ser Tyr Ile Ser | Glu Gly Ala Phe Glu Gly |     |
| 185                                 | 190                     | 195 |
| Leu Ser Asn Leu Arg Tyr Leu Asn Leu | Ala Met Cys Asn Leu Arg |     |
| 200                                 | 205                     | 210 |
| Glu Ile Pro Asn Leu Thr Pro Leu Ile | Lys Leu Asp Glu Leu Asp |     |
| 215                                 | 220                     | 225 |
| Leu Ser Gly Asn His Leu Ser Ala Ile | Arg Pro Gly Ser Phe Gln |     |
| 230                                 | 235                     | 240 |
| Gly Leu Met His Leu Gln Lys Leu Trp | Met Ile Gln Ser Gln Ile |     |
| 245                                 | 250                     | 255 |
| Gln Val Ile Glu Arg Asn Ala Phe Asp | Asn Leu Gln Ser Leu Val |     |
| 260                                 | 265                     | 270 |
| Glu Ile Asn Leu Ala His Asn Asn Leu | Thr Leu Leu Pro His Asp |     |
| 275                                 | 280                     | 285 |
| Leu Phe Thr Pro Leu His His Leu Glu | Arg Ile His Leu His His |     |
| 290                                 | 295                     | 300 |
| Asn Pro Trp Asn Cys Asn Cys Asp Ile | Leu Trp Leu Ser Trp Trp |     |
| 305                                 | 310                     | 315 |
| Ile Lys Asp Met Ala Pro Ser Asn Thr | Ala Cys Cys Ala Arg Cys |     |
| 320                                 | 325                     | 330 |
| Asn Thr Pro Pro Asn Leu Lys Gly Arg | Tyr Ile Gly Glu Leu Asp |     |
| 335                                 | 340                     | 345 |
| Gln Asn Tyr Phe Thr Cys Tyr Ala Pro | Val Ile Val Glu Pro Pro |     |
| 350                                 | 355                     | 360 |
| Ala Asp Leu Asn Val Thr Glu Gly Met | Ala Ala Glu Leu Lys Cys |     |
| 365                                 | 370                     | 375 |
| Arg Ala Ser Thr Ser Leu Thr Ser Val | Ser Trp Ile Thr Pro Asn |     |
| 380                                 | 385                     | 390 |
| Gly Thr Val Met Thr His Gly Ala Tyr | Lys Val Arg Ile Ala Val |     |
| 395                                 | 400                     | 405 |
| Leu Ser Asp Gly Thr Leu Asn Phe Thr | Asn Val Thr Val Gln Asp |     |
| 410                                 | 415                     | 420 |

FOET 70-84250660

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 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
 515 520 525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
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 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
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05505348.07.1301



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<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg  
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
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Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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|                                                             |                         |     |
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| 215                                                         | 220                     | 225 |
| Lys Ile Lys Asn Val Asp Gly Leu Thr                         | Phe Gln Gly Leu Gly Ala |     |
| 230                                                         | 235                     | 240 |
| Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met |                         |     |
| 245                                                         | 250                     | 255 |
| Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu |                         |     |
| 260                                                         | 265                     | 270 |
| Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly |                         |     |
| 275                                                         | 280                     | 285 |
| Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn |                         |     |
| 290                                                         | 295                     | 300 |
| Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu |                         |     |
| 305                                                         | 310                     | 315 |
| Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser |                         |     |
| 320                                                         | 325                     | 330 |
| Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn |                         |     |
| 335                                                         | 340                     | 345 |
| Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser |                         |     |
| 350                                                         | 355                     | 360 |
| Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile |                         |     |
| 365                                                         | 370                     | 375 |
| Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg |                         |     |
| 380                                                         | 385                     | 390 |
| Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala |                         |     |
| 395                                                         | 400                     | 405 |
| Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn |                         |     |
| 410                                                         | 415                     | 420 |
| Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys |                         |     |
| 425                                                         | 430                     | 435 |
| Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys |                         |     |
| 440                                                         | 445                     | 450 |
| Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln |                         |     |
| 455                                                         | 460                     | 465 |
| Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly |                         |     |
| 470                                                         | 475                     | 480 |

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T06T20-84E50660

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| Arg Ser Ile Phe | Ala Val Ser Pro Asp | Gly Phe Val Cys Asp Asp |
| 485             |                     | 490 495                 |
| Phe Pro Lys Pro | Gln Ile Thr Val Gln | Pro Glu Thr Gln Ser Ala |
| 500             |                     | 505 510 515             |
| Ile Lys Gly Ser | Asn Leu Ser Phe Ile | Cys Ser Ala Ala Ser Ser |
| 515             |                     | 520 525                 |
| Ser Asp Ser Pro | Met Thr Phe Ala Trp | Lys Lys Asp Asn Glu Leu |
| 530             |                     | 535 540                 |
| Leu His Asp Ala | Glu Met Glu Asn Tyr | Ala His Leu Arg Ala Gln |
| 545             |                     | 550 555                 |
| Gly Gly Glu Val | Met Glu Tyr Thr Thr | Ile Leu Arg Leu Arg Glu |
| 560             |                     | 565 570                 |
| Val Glu Phe Ala | Ser Glu Gly Lys Tyr | Gln Cys Val Ile Ser Asn |
| 575             |                     | 580 585                 |
| His Phe Gly Ser | Ser Tyr Ser Val Lys | Ala Lys Leu Thr Val Asn |
| 590             |                     | 595 600                 |
| Met Leu Pro Ser | Phe Thr Lys Thr Pro | Met Asp Leu Thr Ile Arg |
| 605             |                     | 610 615                 |
| Ala Gly Ala Met | Ala Arg Leu Glu Cys | Ala Ala Val Gly His Pro |
| 620             |                     | 625 630                 |
| Ala Pro Gln Ile | Ala Trp Gln Lys Asp | Gly Gly Thr Asp Phe Pro |
| 635             |                     | 640 645                 |
| Ala Ala Arg Glu | Arg Arg Met His Val | Met Pro Glu Asp Asp Val |
| 650             |                     | 655 660                 |
| Phe Phe Ile Val | Asp Val Lys Ile Glu | Asp Ile Gly Val Tyr Ser |
| 665             |                     | 670 675                 |
| Cys Thr Ala Gln | Asn Ser Ala Gly Ser | Ile Ser Ala Asn Ala Thr |
| 680             |                     | 685 690                 |
| Leu Thr Val Leu | Glu Thr Pro Ser Phe | Leu Arg Pro Leu Leu Asp |
| 695             |                     | 700 705                 |
| Arg Thr Val Thr | Lys Gly Glu Thr Ala | Val Leu Gln Cys Ile Ala |
| 710             |                     | 715 720                 |
| Gly Gly Ser Pro | Pro Pro Lys Leu Asn | Trp Thr Lys Asp Asp Ser |
| 725             |                     | 730 735                 |
| Pro Leu Val Val | Thr Glu Arg His Phe | Phe Ala Ala Gly Asn Gln |
| 740             |                     | 745 750                 |

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 F01E120-84E50660

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|
| Leu | Leu | Ile | Ile | Val | Asp | Ser | Asp | Val | Ser | Asp | Ala | Gly | Lys | Tyr | 755 | 760  | 765  |
| Thr | Cys | Glu | Met | Ser | Asn | Thr | Leu | Gly | Thr | Glu | Arg | Gly | Asn | Val | 770 | 775  | 780  |
| Arg | Leu | Ser | Val | Ile | Pro | Thr | Pro | Thr | Cys | Asp | Ser | Pro | Gln | Met | 785 | 790  | 795  |
| Thr | Ala | Pro | Ser | Leu | Asp | Asp | Asp | Gly | Trp | Ala | Thr | Val | Gly | Val | 800 | 805  | 810  |
| Val | Ile | Ile | Ala | Val | Val | Cys | Cys | Val | Val | Gly | Thr | Ser | Leu | Val | 815 | 820  | 825  |
| Trp | Val | Val | Ile | Ile | Tyr | His | Thr | Arg | Arg | Arg | Asn | Glu | Asp | Cys | 830 | 835  | 840  |
| Ser | Ile | Thr | Asn | Thr | Asp | Glu | Thr | Asn | Leu | Pro | Ala | Asp | Ile | Pro | 845 | 850  | 855  |
| Ser | Tyr | Leu | Ser | Ser | Gln | Gly | Thr | Leu | Ala | Asp | Arg | Gln | Asp | Gly | 860 | 865  | 870  |
| Tyr | Val | Ser | Ser | Glu | Ser | Gly | Ser | His | His | Gln | Phe | Val | Thr | Ser | 875 | 880  | 885  |
| Ser | Gly | Ala | Gly | Phe | Phe | Leu | Pro | Gln | His | Asp | Ser | Ser | Gly | Thr | 890 | 895  | 900  |
| Cys | His | Ile | Asp | Asn | Ser | Ser | Glu | Ala | Asp | Val | Glu | Ala | Ala | Thr | 905 | 910  | 915  |
| Asp | Leu | Phe | Leu | Cys | Pro | Phe | Leu | Gly | Ser | Thr | Gly | Pro | Met | Tyr | 920 | 925  | 930  |
| Leu | Lys | Gly | Asn | Val | Tyr | Gly | Ser | Asp | Pro | Phe | Glu | Thr | Tyr | His | 935 | 940  | 945  |
| Thr | Gly | Cys | Ser | Pro | Asp | Pro | Arg | Thr | Val | Leu | Met | Asp | His | Tyr | 950 | 955  | 960  |
| Glu | Pro | Ser | Tyr | Ile | Lys | Lys | Lys | Glu | Cys | Tyr | Pro | Cys | Ser | His | 965 | 970  | 975  |
| Pro | Ser | Glu | Glu | Ser | Cys | Glu | Arg | Ser | Phe | Ser | Asn | Ile | Ser | Trp | 980 | 985  | 990  |
| Pro | Ser | His | Val | Arg | Lys | Leu | Leu | Asn | Thr | Ser | Tyr | Ser | His | Asn | 995 | 1000 | 1005 |
| Glu | Gly | Pro | Gly | Met | Lys | Asn | Leu | Cys | Leu | Asn | Lys | Ser | Ser | Leu |     |      |      |

TOEFL® PRACTICE

| 1010                                                        | 1015 | 1020 |
|-------------------------------------------------------------|------|------|
| Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn |      |      |
| 1025                                                        | 1030 | 1035 |
| Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu |      |      |
| 1040                                                        | 1045 | 1050 |
| Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg |      |      |
| 1055                                                        | 1060 | 1065 |
| Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly |      |      |
| 1070                                                        | 1075 | 1080 |
| Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn |      |      |
| 1085                                                        | 1090 | 1095 |
| His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro |      |      |
| 1100                                                        | 1105 | 1110 |
| Asn Phe Gln Ser Tyr Asp Leu Asp Thr                         |      |      |
| 1115                                                        |      |      |

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&lt;400&gt; 295

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&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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TOE120"84E50660



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<223> Synthetic Oligonucleotide Probe

ccccatgtgt ccatgactgt tccc 24

<211> 45

<213> Artificial Sequence

## <223> Synthetic Oligonucleotide Probe

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<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

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| Met | Asp | Phe | Leu | Leu | Ala | Leu | Val | Leu | Val | Ser | Ser | Leu | Tyr | Leu | 1   | 5   | 10  | 15 |
| Gln | Ala | Ala | Ala | Glu | Phe | Asp | Gly | Arg | Trp | Pro | Arg | Gln | Ile | Val | 20  | 25  | 30  |    |
| Ser | Ser | Ile | Gly | Leu | Cys | Arg | Tyr | Gly | Gly | Arg | Ile | Asp | Cys | Cys | 35  | 40  | 45  |    |
| Trp | Gly | Trp | Ala | Arg | Gln | Ser | Trp | Gly | Gln | Cys | Gln | Pro | Val | Cys | 50  | 55  | 60  |    |
| Gln | Pro | Arg | Cys | Lys | His | Gly | Glu | Cys | Ile | Gly | Pro | Asn | Lys | Cys | 65  | 70  | 75  |    |
| Lys | Cys | His | Pro | Gly | Tyr | Ala | Gly | Lys | Thr | Cys | Asn | Gln | Asp | Leu | 80  | 85  | 90  |    |
| Asn | Glu | Cys | Gly | Leu | Lys | Pro | Arg | Pro | Cys | Lys | His | Arg | Cys | Met | 95  | 100 | 105 |    |
| Asn | Thr | Tyr | Gly | Ser | Tyr | Lys | Cys | Tyr | Cys | Leu | Asn | Gly | Tyr | Met | 110 | 115 | 120 |    |
| Leu | Met | Pro | Asp | Gly | Ser | Cys | Ser | Ser | Ala | Leu | Thr | Cys | Ser | Met | 125 | 130 | 135 |    |
| Ala | Asn | Cys | Gln | Tyr | Gly | Cys | Asp | Val | Val | Lys | Gly | Gln | Ile | Arg | 140 | 145 | 150 |    |
| Cys | Gln | Cys | Pro | Ser | Pro | Gly | Leu | His | Leu | Ala | Pro | Asp | Gly | Arg | 155 | 160 | 165 |    |

05905348 "071301" 05905348

|                 |                     |                         |
|-----------------|---------------------|-------------------------|
| Thr Cys Val Asp | Val Asp Glu Cys Ala | Thr Gly Arg Ala Ser Cys |
| 170             |                     | 175 180                 |
| Pro Arg Phe Arg | Gln Cys Val Asn Thr | Phe Gly Ser Tyr Ile Cys |
| 185             |                     | 190 195                 |
| Lys Cys His Lys | Gly Phe Asp Leu Met | Tyr Ile Gly Gly Lys Tyr |
| 200             |                     | 205 210                 |
| Gln Cys His Asp | Ile Asp Glu Cys Ser | Leu Gly Gln Tyr Gln Cys |
| 215             |                     | 220 225                 |
| Ser Ser Phe Ala | Arg Cys Tyr Asn Val | Arg Gly Ser Tyr Lys Cys |
| 230             |                     | 235 240                 |
| Lys Cys Lys Glu | Gly Tyr Gln Gly Asp | Gly Leu Thr Cys Val Tyr |
| 245             |                     | 250 255                 |
| Ile Pro Lys Val | Met Ile Glu Pro Ser | Gly Pro Ile His Val Pro |
| 260             |                     | 265 270                 |
| Lys Gly Asn Gly | Thr Ile Leu Lys Gly | Asp Thr Gly Asn Asn Asn |
| 275             |                     | 280 285                 |
| Trp Ile Pro Asp | Val Gly Ser Thr Trp | Trp Pro Pro Lys Thr Pro |
| 290             |                     | 295 300                 |
| Tyr Ile Pro Pro | Ile Ile Thr Asn Arg | Pro Thr Ser Lys Pro Thr |
| 305             |                     | 310 315                 |
| Thr Arg Pro Thr | Pro Lys Pro Thr Pro | Ile Pro Thr Pro Pro Pro |
| 320             |                     | 325 330                 |
| Pro Pro Pro Leu | Pro Thr Glu Leu Arg | Thr Pro Leu Pro Pro Thr |
| 335             |                     | 340 345                 |
| Thr Pro Glu Arg | Pro Thr Thr Gly Leu | Thr Thr Ile Ala Pro Ala |
| 350             |                     | 355 360                 |
| Ala Ser Thr Pro | Pro Gly Gly Ile Thr | Val Asp Asn Arg Val Gln |
| 365             |                     | 370 375                 |
| Thr Asp Pro Gln | Lys Pro Arg Gly Asp | Val Phe Ser Val Leu Val |
| 380             |                     | 385 390                 |
| His Ser Cys Asn | Phe Asp His Gly Leu | Cys Gly Trp Ile Arg Glu |
| 395             |                     | 400 405                 |
| Lys Asp Asn Asp | Leu His Trp Glu Pro | Ile Arg Asp Pro Ala Gly |
| 410             |                     | 415 420                 |
| Gly Gln Tyr Leu | Thr Val Ser Ala Ala | Lys Ala Pro Gly Gly Lys |

099548-0130

|                                                             |     |     |
|-------------------------------------------------------------|-----|-----|
| 425                                                         | 430 | 435 |
| Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly |     |     |
| 440                                                         | 445 | 450 |
| Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser |     |     |
| 455                                                         | 460 | 465 |
| Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala |     |     |
| 470                                                         | 475 | 480 |
| Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln |     |     |
| 485                                                         | 490 | 495 |
| Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg     |     |     |
| 500                                                         | 505 |     |

<210> 316  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

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<210> 317  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 317  
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<210> 318  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 318  
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<210> 319  
 <211> 2110  
 <212> DNA

090548.071301

<213> Homo Sapien

<400> 319

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catggcgctc gaggtcaggc cctctacctc cccgtccact atggcttcca 200
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caatgccccaa atacttactg ggctctgtga ataagtctgt ggttctctgac 300
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tatcaacca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400
acattcaggg aaatggaact ctatctgccg gtcagaagat acaagtcacg 450
gttgatgatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500
ggctgtggag tatgtgggga acatgacctc gacatgccat gtggaagggg 550
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09905348.071304

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 tttattagt ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900  
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 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Leu | Lys | Val | Phe | Thr | Thr | Phe | Leu | Ser | Phe | Ala | Thr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Cys | Ser | Gly | Leu | Lys | Val | Thr | Val | Pro | Ser | His | Thr | Val | His |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Arg | Gly | Gln | Ala | Leu | Tyr | Leu | Pro | Val | His | Tyr | Gly | Phe |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Pro | Ala | Ser | Asp | Ile | Gln | Ile | Ile | Trp | Leu | Phe | Glu | Arg |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |

0905348-01301

|                 |                                             |     |     |     |
|-----------------|---------------------------------------------|-----|-----|-----|
| Pro His Thr Met | Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser | 65  | 70  | 75  |
| Val Val Pro Asp | Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro | 80  | 85  | 90  |
| Pro Asn Ala Ser | Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu | 95  | 100 | 105 |
| Gly Asn Tyr Ile | Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu | 110 | 115 | 120 |
| Ser Ala Ser Gln | Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr | 125 | 130 | 135 |
| Lys Pro Val Val | Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr | 140 | 145 | 150 |
| Val Gly Asn Met | Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg | 155 | 160 | 165 |
| Leu Ala Tyr Gln | Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser | 170 | 175 | 180 |
| Ser Thr Tyr Ser | Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala | 185 | 190 | 195 |
| Pro Val Thr Lys | Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg | 200 | 205 | 210 |
| Asn Pro Val Ser | Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile | 215 | 220 | 225 |
| Tyr Tyr Gly Pro | Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu | 230 | 235 | 240 |
| Lys Val Gly Glu | Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu | 245 | 250 | 255 |
| Phe Asp Cys Ser | Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp | 260 | 265 | 270 |
| Ile Arg Arg Thr | Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro | 275 | 280 | 285 |
| Arg Leu Glu Val | Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp | 290 | 295 | 300 |
| Tyr Val Cys Cys | Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu | 305 | 310 | 315 |
| Thr His Phe Thr | Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu |     |     |     |

0990548-071341  
F06T120-B4E50660

|                                                             |     |     |
|-------------------------------------------------------------|-----|-----|
| 320                                                         | 325 | 330 |
| Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly |     |     |
| 335                                                         | 340 | 345 |
| Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp |     |     |
| 350                                                         | 355 | 360 |
| Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly |     |     |
| 365                                                         | 370 | 375 |
| Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His |     |     |
| 380                                                         | 385 | 390 |
| Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe |     |     |
| 395                                                         | 400 | 405 |
| Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro |     |     |
| 410                                                         | 415 | 420 |
| Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr |     |     |
| 425                                                         | 430 | 435 |
| Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu |     |     |
| 440                                                         | 445 | 450 |

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gacacctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

TOET 20 84E50650

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
 tggatgatag aattttatgc cccgtgggtgc cctgcttgctc aaaatcttca 200  
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250  
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 ataactgctc ttctactat ttatcattgt aaagatgggtg aatttaggcg 350  
 ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400  
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 ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgcag 650  
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 aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750  
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 ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

0990348-02301



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 aatttacatt tccaagtat tgcattattg aggtatttaa gaagattatt 1200  
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0990348-021301

aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly  
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln  
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp  
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His  
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile  
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys  
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

090548-071301  
FOET 20-84E50660

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 215 |     | 220 |     | 225 |     |     |     |     |     |     |     |     |     |
| Ser | Glu | Ser | Ala | Gln | Pro | Leu | Lys | Lys | Val | Glu | Glu | Glu | Gln | Glu |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Asp | Glu | Glu | Asp | Val | Ser | Glu | Glu | Glu | Ala | Glu | Ser | Lys | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Gly | Thr | Asn | Lys | Asp | Phe | Pro | Gln | Asn | Ala | Ile | Arg | Gln | Arg | Ser |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |
| Leu | Gly | Pro | Ser | Leu | Ala | Thr | Asp | Lys | Ser |     |     |     |     |     |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     |     |

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

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&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

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&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

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&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<400> 329

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<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

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<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

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 acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
 ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250  
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 ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400  
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 ggacccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650  
 caatgctgag tgtggatgac tgctttggga tgggccgctc ggctacaat 700  
 gaaggggact attatcatatc ggtgttgtgg atggagcagg tgctaaagca 750

090549-0101  
 T00120-BHE50660

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<213> Homo Sapien

<400> 332

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35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp  
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val  
80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu  
95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg  
110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala  
125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile  
140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser  
155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly  
170 175 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln  
185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu  
200 205 210

TEEF20"34E5D55D

|     |     |     |     |            |     |     |     |     |            |     |     |     |     |            |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Asp | Tyr | Leu | Ser | Tyr<br>215 | Ala | Val | Phe | Gln | Leu<br>220 | Gly | Asp | Leu | His | Arg<br>225 |
| Ala | Leu | Glu | Leu | Thr<br>230 | Arg | Arg | Leu | Leu | Ser<br>235 | Leu | Asp | Pro | Ser | His<br>240 |
| Glu | Arg | Ala | Gly | Gly<br>245 | Asn | Leu | Arg | Tyr | Phe<br>250 | Glu | Gln | Leu | Leu | Glu<br>255 |
| Glu | Glu | Arg | Glu | Lys<br>260 | Thr | Leu | Thr | Asn | Gln<br>265 | Thr | Glu | Ala | Glu | Leu<br>270 |
| Ala | Thr | Pro | Glu | Gly<br>275 | Ile | Tyr | Glu | Arg | Pro<br>280 | Val | Asp | Tyr | Leu | Pro<br>285 |
| Glu | Arg | Asp | Val | Tyr<br>290 | Glu | Ser | Leu | Cys | Arg<br>295 | Gly | Glu | Gly | Val | Lys<br>300 |
| Leu | Thr | Pro | Arg | Arg<br>305 | Gln | Lys | Arg | Leu | Phe<br>310 | Cys | Arg | Tyr | His | His<br>315 |
| Gly | Asn | Arg | Ala | Pro<br>320 | Gln | Leu | Leu | Ile | Ala<br>325 | Pro | Phe | Lys | Glu | Glu<br>330 |
| Asp | Glu | Trp | Asp | Ser<br>335 | Pro | His | Ile | Val | Arg<br>340 | Tyr | Tyr | Asp | Val | Met<br>345 |
| Ser | Asp | Glu | Glu | Ile<br>350 | Glu | Arg | Ile | Lys | Glu<br>355 | Ile | Ala | Lys | Pro | Lys<br>360 |
| Leu | Ala | Arg | Ala | Thr<br>365 | Val | Arg | Asp | Pro | Lys<br>370 | Thr | Gly | Val | Leu | Thr<br>375 |
| Val | Ala | Ser | Tyr | Arg<br>380 | Val | Ser | Lys | Ser | Ser<br>385 | Trp | Leu | Glu | Glu | Asp<br>390 |
| Asp | Asp | Pro | Val | Val<br>395 | Ala | Arg | Val | Asn | Arg<br>400 | Arg | Met | Gln | His | Ile<br>405 |
| Thr | Gly | Leu | Thr | Val<br>410 | Lys | Thr | Ala | Glu | Leu<br>415 | Leu | Gln | Val | Ala | Asn<br>420 |
| Tyr | Gly | Val | Gly | Gly<br>425 | Gln | Tyr | Glu | Pro | His<br>430 | Phe | Asp | Phe | Ser | Arg<br>435 |
| Arg | Pro | Phe | Asp | Ser<br>440 | Gly | Leu | Lys | Thr | Glu<br>445 | Gly | Asn | Arg | Leu | Ala<br>450 |
| Thr | Phe | Leu | Asn | Tyr<br>455 | Met | Ser | Asp | Val | Glu<br>460 | Ala | Gly | Gly | Ala | Thr<br>465 |
| Val | Phe | Pro | Asp | Leu<br>470 | Gly | Ala | Ala | Ile | Trp<br>475 | Pro | Lys | Lys | Gly | Thr<br>480 |

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
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<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Leu | Ser | Ser | Leu | Leu | Ala | Leu | Leu | Arg | Pro | Ala | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Leu | Gly | Leu | Ser | Leu | Gly | Cys | Ser | Leu | Ser | Leu | Leu | Arg |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Trp | Ile | Gln | Gly | Glu | Gly | Glu | Asp | Pro | Cys | Val | Glu | Ala |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Glu | Arg | Gly | Gly | Pro | Gln | Asn | Pro | Asp | Ser | Arg | Ala | Arg |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Gln | Ser | Asp | Glu | Asp | Phe | Lys | Pro | Arg | Ile | Val | Pro | Tyr |
|     |     |     | 65  |     |     |     |     |     | 70  |     |     |     |     | 75  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Arg | Asp | Pro | Asn | Lys | Pro | Tyr | Lys | Lys | Val | Leu | Arg | Thr | Arg |
|     |     |     | 80  |     |     |     |     |     | 85  |     |     |     |     | 90  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Gln | Thr | Glu | Leu | Gly | Ser | Arg | Glu | Arg | Leu | Leu | Val | Ala |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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|                 |                     |                 |         |  |     |
|-----------------|---------------------|-----------------|---------|--|-----|
|                 | 95                  |                 | 100     |  | 105 |
| Val Leu Thr Ser | Arg Ala Thr Leu Ser | Thr Leu Ala Val | Ala Val |  |     |
|                 | 110                 |                 | 115     |  | 120 |
| Asn Arg Thr Val | Ala His His Phe Pro | Arg Leu Leu Tyr | Phe Thr |  |     |
|                 | 125                 |                 | 130     |  | 135 |
| Gly Gln Arg Gly | Ala Arg Ala Pro Ala | Gly Met Gln Val | Val Ser |  |     |
|                 | 140                 |                 | 145     |  | 150 |
| His Gly Asp Glu | Arg Pro Ala Trp Leu | Met Ser Glu Thr | Leu Arg |  |     |
|                 | 155                 |                 | 160     |  | 165 |
| His Leu His Thr | His Phe Gly Ala Asp | Tyr Asp Trp Phe | Phe Ile |  |     |
|                 | 170                 |                 | 175     |  | 180 |
| Met Gln Asp Asp | Thr Tyr Val Gln Ala | Pro Arg Leu Ala | Ala Leu |  |     |
|                 | 185                 |                 | 190     |  | 195 |
| Ala Gly His Leu | Ser Ile Asn Gln Asp | Leu Tyr Leu Gly | Arg Ala |  |     |
|                 | 200                 |                 | 205     |  | 210 |
| Glu Glu Phe Ile | Gly Ala Gly Glu Gln | Ala Arg Tyr Cys | His Gly |  |     |
|                 | 215                 |                 | 220     |  | 225 |
| Gly Phe Gly Tyr | Leu Leu Ser Arg Ser | Leu Leu Leu Arg | Leu Arg |  |     |
|                 | 230                 |                 | 235     |  | 240 |
| Pro His Leu Asp | Gly Cys Arg Gly Asp | Ile Leu Ser Ala | Arg Pro |  |     |
|                 | 245                 |                 | 250     |  | 255 |
| Asp Glu Trp Leu | Gly Arg Cys Leu Ile | Asp Ser Leu Gly | Val Gly |  |     |
|                 | 260                 |                 | 265     |  | 270 |
| Cys Val Ser Gln | His Gln Gly Gln Gln | Tyr Arg Ser Phe | Glu Leu |  |     |
|                 | 275                 |                 | 280     |  | 285 |
| Ala Lys Asn Arg | Asp Pro Glu Lys Glu | Gly Ser Ser Ala | Phe Leu |  |     |
|                 | 290                 |                 | 295     |  | 300 |
| Ser Ala Phe Ala | Val His Pro Val Ser | Glu Gly Thr Leu | Met Tyr |  |     |
|                 | 305                 |                 | 310     |  | 315 |
| Arg Leu His Lys | Arg Phe Ser Ala Leu | Glu Leu Glu Arg | Ala Tyr |  |     |
|                 | 320                 |                 | 325     |  | 330 |
| Ser Glu Ile Glu | Gln Leu Gln Ala Gln | Ile Arg Asn Leu | Thr Val |  |     |
|                 | 335                 |                 | 340     |  | 345 |
| Leu Thr Pro Glu | Gly Glu Ala Gly Leu | Ser Trp Pro Val | Gly Leu |  |     |
|                 | 350                 |                 | 355     |  | 360 |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Pro | Phe | Thr | Pro | His | Ser | Arg | Phe | Glu | Val | Leu | Gly | Trp | 365 | 370 | 375 |
| Asp | Tyr | Phe | Thr | Glu | Gln | His | Thr | Phe | Ser | Cys | Ala | Asp | Gly | Ala | 380 | 385 | 390 |
| Pro | Lys | Cys | Pro | Leu | Gln | Gly | Ala | Ser | Arg | Ala | Asp | Val | Gly | Asp | 395 | 400 | 405 |
| Ala | Leu | Glu | Thr | Ala | Leu | Glu | Gln | Leu | Asn | Arg | Arg | Tyr | Gln | Pro | 410 | 415 | 420 |
| Arg | Leu | Arg | Phe | Gln | Lys | Gln | Arg | Leu | Leu | Asn | Gly | Tyr | Arg | Arg | 425 | 430 | 435 |
| Phe | Asp | Pro | Ala | Arg | Gly | Met | Glu | Tyr | Thr | Leu | Asp | Leu | Leu | Leu | 440 | 445 | 450 |
| Glu | Cys | Val | Thr | Gln | Arg | Gly | His | Arg | Arg | Ala | Leu | Ala | Arg | Arg | 455 | 460 | 465 |
| Val | Ser | Leu | Leu | Arg | Pro | Leu | Ser | Arg | Val | Glu | Ile | Leu | Pro | Met | 470 | 475 | 480 |
| Pro | Tyr | Val | Thr | Glu | Ala | Thr | Arg | Val | Gln | Leu | Val | Leu | Pro | Leu | 485 | 490 | 495 |
| Leu | Val | Ala | Glu | Ala | Ala | Ala | Ala | Pro | Ala | Phe | Leu | Glu | Ala | Phe | 500 | 505 | 510 |
| Ala | Ala | Asn | Val | Leu | Glu | Pro | Arg | Glu | His | Ala | Leu | Leu | Thr | Leu | 515 | 520 | 525 |
| Leu | Leu | Val | Tyr | Gly | Pro | Arg | Glu | Gly | Gly | Arg | Gly | Ala | Pro | Asp | 530 | 535 | 540 |
| Pro | Phe | Leu | Gly | Val | Lys | Ala | Ala | Ala | Ala | Glu | Leu | Glu | Arg | Arg | 545 | 550 | 555 |
| Tyr | Pro | Gly | Thr | Arg | Leu | Ala | Trp | Leu | Ala | Val | Arg | Ala | Glu | Ala | 560 | 565 | 570 |
| Pro | Ser | Gln | Val | Arg | Leu | Met | Asp | Val | Val | Ser | Lys | Lys | His | Pro | 575 | 580 | 585 |
| Val | Asp | Thr | Leu | Phe | Phe | Leu | Thr | Thr | Val | Trp | Thr | Arg | Pro | Gly | 590 | 595 | 600 |
| Pro | Glu | Val | Leu | Asn | Arg | Cys | Arg | Met | Asn | Ala | Ile | Ser | Gly | Trp | 605 | 610 | 615 |
| Gln | Ala | Phe | Phe | Pro | Val | His | Phe | Gln | Glu | Phe | Asn | Pro | Ala | Leu | 620 | 625 | 630 |

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 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
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&lt;211&gt; 1572

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 340

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 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccacatgag 200  
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 gcaaatgata tctctagttg tgaatttggt attaaagtaa aacttttagc 1450  
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0905343.071301

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| Met | Leu | Ser | Glu | Ser | Ser | Ser | Phe | Leu | Lys | Gly | Val | Met | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Ser | Ile | Phe | Cys | Ala | Leu | Ile | Thr | Met | Leu | Gly | His | Ile | Arg | Ile |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Gly | His | Gly | Asn | Arg | Met | His | His | His | Glu | His | His | His | Leu | Gln |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Ala | Pro | Asn | Lys | Glu | Asp | Ile | Leu | Lys | Ile | Ser | Glu | Asp | Glu | Arg |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Met | Glu | Leu | Ser | Lys | Ser | Phe | Arg | Val | Tyr | Cys | Ile | Ile | Leu | Val |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Lys | Pro | Lys | Asp | Val | Ser | Leu | Trp | Ala | Ala | Val | Lys | Glu | Thr | Trp |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Thr | Lys | His | Cys | Asp | Lys | Ala | Glu | Phe | Phe | Ser | Ser | Glu | Asn | Val |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Lys | Val | Phe | Glu | Ser | Ile | Asn | Met | Asp | Thr | Asn | Asp | Met | Trp | Leu |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |
| Met | Met | Arg | Lys | Ala | Tyr | Lys | Tyr | Ala | Phe | Asp | Lys | Tyr | Arg | Asp |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Gln | Tyr | Asn | Trp | Phe | Phe | Leu | Ala | Arg | Pro | Thr | Thr | Phe | Ala | Ile |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |
| Ile | Glu | Asn | Leu | Lys | Tyr | Phe | Leu | Leu | Lys | Lys | Asp | Pro | Ser | Gln |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |
| Pro | Phe | Tyr | Leu | Gly | His | Thr | Ile | Lys | Ser | Gly | Asp | Leu | Glu | Tyr |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |
| Val | Gly | Met | Glu | Gly | Gly | Ile | Val | Leu | Ser | Val | Glu | Ser | Met | Lys |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |
| Arg | Leu | Asn | Ser | Leu | Leu | Asn | Ile | Pro | Glu | Lys | Cys | Pro | Glu | Gln |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |
| Gly | Gly | Met | Ile | Trp | Lys | Ile | Ser | Glu | Asp | Lys | Gln | Leu | Ala | Val |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |
| Cys | Leu | Lys | Tyr | Ala | Gly | Val | Phe | Ala | Glu | Asn | Ala | Glu | Asp | Ala |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Gly | Lys | Asp | Val | Phe | Asn | Thr | Lys | Ser | Val | Gly | Leu | Ser | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Lys | Glu | Ala | Met | Thr | Tyr | His | Pro | Asn | Gln | Val | Val | Glu | Gly | Cys |

TOET 20-84E50660



Asp Asn Asp

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T0E720-B4E50650

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| Met | Asn | Ser | Ser | Lys | Ser | Ser | Glu | Thr | Gln | Cys | Thr | Glu | Arg | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Cys | Phe | Ser | Ser | Gln | Met | Phe | Leu | Trp | Thr | Val | Ala | Gly | Ile | Pro |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |  |
| Ile | Leu | Phe | Leu | Ser | Ala | Cys | Phe | Ile | Thr | Arg | Cys | Val | Val | Thr |  |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |  |
| Phe | Arg | Ile | Phe | Gln | Thr | Cys | Asp | Glu | Lys | Lys | Phe | Gln | Leu | Pro |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |  |
| Glu | Asn | Phe | Thr | Glu | Leu | Ser | Cys | Tyr | Asn | Tyr | Gly | Ser | Gly | Ser |  |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |  |
| Val | Lys | Asn | Cys | Cys | Pro | Leu | Asn | Trp | Glu | Tyr | Phe | Gln | Ser | Ser |  |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |  |
| Cys | Tyr | Phe | Phe | Ser | Thr | Asp | Thr | Ile | Ser | Trp | Ala | Leu | Ser | Leu |  |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |  |
| Lys | Asn | Cys | Ser | Ala | Met | Gly | Ala | His | Leu | Val | Val | Ile | Asn | Ser |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |  |
| Gln | Glu | Glu | Gln | Glu | Phe | Leu | Ser | Tyr | Lys | Lys | Pro | Lys | Met | Arg |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |  |
| Glu | Phe | Phe | Ile | Gly | Leu | Ser | Asp | Gln | Val | Val | Glu | Gly | Gln | Trp |  |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |  |
| Gln | Trp | Val | Asp | Gly | Thr | Pro | Leu | Thr | Lys | Ser | Leu | Ser | Phe | Trp |  |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |  |
| Asp | Val | Gly | Glu | Pro | Asn | Asn | Ile | Ala | Thr | Leu | Glu | Asp | Cys | Ala |  |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |  |

0905050600-20210710

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
 185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
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Asn Pro Leu Asn Lys Gly Lys Ser Leu  
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TOEFL-34E50660

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tgccagctgc atgctgccag tt 22

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atgtcctcca tgcccacgcg 20

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T0E T 20 " 34 50 60

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| Met | Ala | Leu | Arg | Arg | Pro | Pro | Arg | Leu | Arg | Leu | Cys | Ala | Arg | Leu | 1   | 5   | 10  | 15 |
| Pro | Asp | Phe | Phe | Leu | Leu | Leu | Leu | Phe | Arg | Gly | Cys | Leu | Ile | Gly | 20  | 25  | 30  |    |
| Ala | Val | Asn | Leu | Lys | Ser | Ser | Asn | Arg | Thr | Pro | Val | Val | Gln | Glu | 35  | 40  | 45  |    |
| Phe | Glu | Ser | Val | Glu | Leu | Ser | Cys | Ile | Ile | Thr | Asp | Ser | Gln | Thr | 50  | 55  | 60  |    |
| Ser | Asp | Pro | Arg | Ile | Glu | Trp | Lys | Lys | Ile | Gln | Asp | Glu | Gln | Thr | 65  | 70  | 75  |    |
| Thr | Tyr | Val | Phe | Phe | Asp | Asn | Lys | Ile | Gln | Gly | Asp | Leu | Ala | Gly | 80  | 85  | 90  |    |
| Arg | Ala | Glu | Ile | Leu | Gly | Lys | Thr | Ser | Leu | Lys | Ile | Trp | Asn | Val | 95  | 100 | 105 |    |
| Thr | Arg | Arg | Asp | Ser | Ala | Leu | Tyr | Arg | Cys | Glu | Val | Val | Ala | Arg | 110 | 115 | 120 |    |
| Asn | Asp | Arg | Lys | Glu | Ile | Asp | Glu | Ile | Val | Ile | Glu | Leu | Thr | Val | 125 | 130 | 135 |    |
| Gln | Val | Lys | Pro | Val | Thr | Pro | Val | Cys | Arg | Val | Pro | Lys | Ala | Val | 140 | 145 | 150 |    |
| Pro | Val | Gly | Lys | Met | Ala | Thr | Leu | His | Cys | Gln | Glu | Ser | Glu | Gly | 155 | 160 | 165 |    |
| His | Pro | Arg | Pro | His | Tyr | Ser | Trp | Tyr | Arg | Asn | Asp | Val | Pro | Leu | 170 | 175 | 180 |    |
| Pro | Thr | Asp | Ser | Arg | Ala | Asn | Pro | Arg | Phe | Arg | Asn | Ser | Ser | Phe | 185 | 190 | 195 |    |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Leu | Asn | Ser | Glu | Thr | Gly | Thr | Leu | Val | Phe | Thr | Ala | Val | His |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |
| Lys | Asp | Asp | Ser | Gly | Gln | Tyr | Tyr | Cys | Ile | Ala | Ser | Asn | Asp | Ala |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |
| Gly | Ser | Ala | Arg | Cys | Glu | Glu | Gln | Glu | Met | Glu | Val | Tyr | Asp | Leu |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Ile | Gly | Gly | Ile | Ile | Gly | Gly | Val | Leu | Val | Val | Leu | Ala | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Leu | Ala | Leu | Ile | Thr | Leu | Gly | Ile | Cys | Cys | Ala | Tyr | Arg | Arg | Gly |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |
| Tyr | Phe | Ile | Asn | Asn | Lys | Gln | Asp | Gly | Glu | Ser | Tyr | Lys | Asn | Pro |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |
| Gly | Lys | Pro | Asp | Gly | Val | Asn | Tyr | Ile | Arg | Thr | Asp | Glu | Glu | Gly |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |
| Asp | Phe | Arg | His | Lys | Ser | Ser | Phe | Val | Ile |     |     |     |     |     |
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